

From: Chernyshev, Olga
Sent: Friday, January 20, 2006 1:18 PM
To: STIC-Biotech/ChemLib
Subject: 09/612,921, sequence search request

Please search SEQ ID NO: 3 down to 95% identity and also 30 contigs of SEQ ID NO: 3 in regular and pending databases.

Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

RECEIVED
JAN 20 2006
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

This page blank (for notes)

Run on:	January 27, 2006, 18:52:33 ; (without alignments)	Search time 3013 Seconds
Scoring table:	IDENTITY_NUC	AY893100 Synthetic
Gapop 10.0 , Gapext 1.0		
Searched:	5883141 seqs, 28421725653 residues	
Total number of hits satisfying chosen parameters:	11766282	
Minimum DB seq length: 0		
Maximum DB seq length: 200000000		
Post-processing: Maximum Match 0%		
Listing first 300 summaries		
Database :	GenBank	
1: gb_ban:*		
2: gb_fn:*		
3: gb_env:*		
4: gb_om:*		
5: gb_ov:*		
6: gb_pac:*		
7: gb_ph:*		
8: gb_pr:*		
9: gb_rn:*		
10: gb_st:*		
11: gb_By:*		
12: gb_un:*		
13: gb_vl:*		
14: gb_hgt:*		
15: gb_pl:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID
	*	
		Description
1	468	100.0 468 6 BD124061
2	468	100.0 468 6 BD63573
3	468	100.0 468 8 AF230316
4	468	100.0 468 11 AY890616
5	468	100.0 1025 6 AR60872
6	468	100.0 1025 6 AX207818
7	468	100.0 1282 6 BD211434
8	468	100.0 1282 6 AR181994
9	468	100.0 1282 6 AR221128
10	468	100.0 1282 6 AR302956
11	468	100.0 1282 6 AX069307
12	468	100.0 1288 8 AF201830
13	468	100.0 2563 6 AX080389
14	468	100.0 2598 6 AX092420
15	468	100.0 2598 6 AX454730
16	468	100.0 2598 6 AX491208
17	468	100.0 2598 8 AY553117
18	468	100.0 2604 8 HSA242738

19	468	100.0 2613 8 HSA242737	AJ242737 Homo sapi
20	468	100.0 2648 6 BD211435	BD211435 A novel i
21	468	100.0 2648 6 AR181995	AR181995 Sequence
22	468	100.0 2648 6 AR221129	AR221129 Sequence
23	468	100.0 2648 6 AR302957	AR302957 Sequence
24	468	100.0 2648 6 AX069309	AX069309 Sequence
25	468	100.0 2692 8 BC024747	BC024747 Homo sapi
26	468	100.0 2720 8 AF186094	AF186094 Homo sapi
27	466.4	99.7 468 11 AY893100	AY893100 Synthetic
28	465	99.4 465 6 AX080398	AX080398 Sequence
29	457	97.6 2701 6 CQ722801	CQ722801 Sequence
30	354.4	75.7 480 6 AX615571	AX615571 Sequence
31	351.2	75.0 468 6 AX063335	AX063335 Sequence
32	351.2	75.0 471 9 AF220378	AF220378 Mus muscu
33	351.2	75.0 1283 9 AX080395	AX080395 Mus muscu
34	351.2	75.0 1284 6 AX080392	AX080392 Sequence
35	351.2	75.0 1284 9 MMU250429	MMU250429 Mus muscu
36	351.2	75.0 1385 6 BD263375	BD263375 IL-1 rela
37	350.2	74.8 470 6 BD106430	BD106430 Mammalian
38	348.2	74.4 465 6 AX080399	AX080399 Sequence
39	348.2	74.4 243 6 BD214060	BD214060 DNA and p
40	348.2	74.4 243 6 BD211432	BD211432 A novel i
41	243	51.9 47 243 6 AR181992	AR181992 Sequence
42	243	51.9 47 243 6 AR221126	AR221126 Sequence
43	243	51.9 49 243 6 AR302954	AR302954 Sequence
44	243	51.9 49 243 6 AX063304	AX063304 Sequence
45	243	51.9 49 243 6 BD211436	BD211436 A novel i
46	243	51.9 49 243 6 AR181996	AR181996 Sequence
47	243	51.9 49 243 6 AR221127	AR221127 Sequence
48	243	51.9 49 243 6 AR302955	AR302955 Sequence
49	243	51.9 985 6 AX063305	AX063305 Sequence
50	236	50.4 295 6 BD263574	BD263574 IL-1 rela
51	227	48.5 5751 6 AR211436	AR211436 A novel i
52	227	48.5 5751 6 AR181996	AR181996 Sequence
53	227	48.5 5751 6 AR221130	AR221130 Sequence
54	227	48.5 5751 6 AR302958	AR302958 Sequence
55	227	48.5 5751 6 AX063310	AX063310 Sequence
56	227	48.5 6540 6 AX080431	AX080431 Sequence
57	227	48.5 6540 6 HSA271338	AT771338 Homo sapi
58	227	48.5 7604 8 AR216693	AR216693 Homo sapi
59	227	48.5 7605 6 BD211437	BD211437 A novel i
60	227	48.5 7605 6 AR211997	AR211997 Sequence
61	227	48.5 7605 6 AR221131	AR221131 Sequence
62	227	48.5 7605 6 AR302959	AR302959 Sequence
63	227	48.5 7605 6 AX059311	AX059311 Sequence
64	227	48.5 12428 8 AY972853	AY972853 Homo sapi
65	227	48.5 197308 8 AC016724	AC016724 Homo sapi
66	20.8	44.6 382 6 BD263576	BD263576 IL-1 rela
67	17.6	37.7 159314 14 AC122732	AC122732 Mus muscu
68	17.6	37.7 199080 14 AC122732	AC122732 Mouse
69	17.6	37.7 201610 9 AY732430	AY732430 Sequence
70	17.4	37.2 8032 6 AX069334	AX069334 Sequence
71	16.2	34.7 265773 14 AC106686	AC106686 Rattus no
72	16.2	34.7 265773 14 AC106686	AY82232 Macaca fa
73	11.0	23.7 456 6 AX594194	AX594194 Sequence
74	11.0	23.7 534 6 AX594192	AX594192 Sequence
75	11.0	23.7 744 6 AR167150	AR167150 Sequence
76	11.0	23.7 998 6 AR182991	AR182991 Sequence
77	11.0	23.7 998 6 AR182992	AR182992 Sequence
78	11.0	23.7 998 6 AR204382	AR204382 Sequence
79	11.0	23.7 998 6 AR204383	AR204383 Sequence
80	11.0	23.7 998 6 AR207385	AR207385 Sequence
81	11.0	23.7 998 6 AR207386	AR207386 Sequence
82	11.0	23.7 998 6 AX08803	AX08803 Sequence
83	11.0	23.7 998 6 AX08805	AX08805 Sequence
84	11.0	23.7 1008 8 AY29413	AY29413 Homo sapi
85	11.0	23.7 1015 8 AY58846	AY58846 Homo sapi
86	11.0	23.7 1020 6 AX167146	AX167146 Sequence
87	11.0	23.7 1020 6 AX167148	AX167148 Sequence
88	11.0	23.5 462 6 AR105636	AR105636 Sequence
89	11.0	23.5 462 6 BD132523	BD132523 Combinati
90	11.0	23.5 462 6 AR233673	AR233673 Sequence
91	11.0	23.5 474 6 A50276	A50276 Sequence 10

Copyright (c) 1993 - 2006 Compugen Ltd.

92	110.2	23.5	474	6	AR001464	AR001464 Sequence	165	95	20.3	1170	6	AR533682
93	110.2	23.5	474	6	AR055509	AR055509 Sequence	166	94.2	20.1	574	4	S68977
94	110.2	23.5	474	6	AR05392	AR05392 Sequence	167	93.8	20.0	549	4	AR204390
95	110.2	23.5	480	11	AY891321	AY891321 Synthetic	168	93.8	20.0	459	6	AX048819
96	110.2	23.5	480	11	AY891322	AY891322 Synthetic	169	93.8	20.0	459	6	AX167180
97	110.2	23.5	480	11	BT019664	BT019664 Synthetic	170	93.8	20.0	538	6	AM206847
98	110.2	23.5	480	11	BT019665	BT019665 Synthetic	171	93.8	20.0	538	9	AY07184
99	110.2	23.5	507	6	BDD77405	BDD77405 Novel pro	172	93.6	20.0	1874	4	AB005148
100	110.2	23.5	514	6	I42450	I42450 Sequence	173	92.8	19.8	331	6	AX193645
101	110.2	23.5	531	6	A49726	A49726 Sequence	174	92.8	19.8	563	4	PIGTRAP
102	110.2	23.5	531	6	A5044	A5044 Sequence	175	92.2	19.7	520	9	MUSLIRNA
103	110.2	23.5	534	6	AR070658	AR070658 Sequence	176	92.2	19.7	542	9	SG64082
104	110.2	23.5	534	8	HUMLIRNA	HUMLIRNA Human inter	177	92.2	19.7	604	9	AR01795
105	110.2	23.5	540	6	109591	109591 Sequence	178	92.2	19.7	1576	9	MUSLIRNA
106	110.2	23.5	540	6	109592	109592 Sequence	179	92.2	19.7	1876	9	ES5194
107	110.2	23.5	543	6	AR004317	AR004317 Sequence	180	92.2	19.7	1877	9	MUSLIRNA
108	110.2	23.5	578	6	CS047660	CS047660 Sequence	181	92.2	19.7	1940	9	MS4404
109	110.2	23.5	578	6	AR380313	AR380313 Sequence	182	91	19.4	238	9	AK193662
110	110.2	23.5	578	8	HSTLIRNA	HSTLIRNA Human inter	183	90.6	19.4	2470	9	BC042532
111	110.2	23.5	579	6	A50219	A50219 Sequence	184	90.6	19.1	537	6	AK420217
112	110.2	23.5	579	6	AR001465	AR001465 Sequence	185	89.6	19.1	537	9	RATTIRNA
113	110.2	23.5	579	6	AR055510	AR055510 Sequence	186	89.6	19.1	1938	9	BC070930
114	110.2	23.5	579	6	AR055393	AR055393 Sequence	187	88.4	18.9	4	AY577820	Sub
115	110.2	23.5	600	6	108135	108135 Sequence	188	87.6	18.7	483	9	SCROF
116	110.2	23.5	600	6	109594	109594 Sequence	189	85.4	18.2	221	4	AF072476
117	110.2	23.5	600	6	BDD06903	BDD06903 Interleuk	190	84	17.9	218	6	AK193630
118	110.2	23.5	602	6	AR050597	AR050597 Sequence	191	82.8	17.7	12665	6	AK4742
119	110.2	23.5	602	6	AR036273	AR036273 Sequence	192	82.8	17.7	12665	6	BD085857
120	110.2	23.5	602	6	AR049621	AR049621 Sequence	193	82.8	17.7	BD271231	Prediction	
121	110.2	23.5	602	6	AR059551	AR059551 Sequence	194	82.8	17.7	CS108085	Sequence	
122	110.2	23.5	602	8	HUMLIRNA	HUMLIRNA Human inter	195	82.8	17.7	12665	6	AR087066
123	110.2	23.5	603	6	AR033238	AR033238 Sequence	196	82.8	17.7	12665	6	AR493824
124	110.2	23.5	603	8	HSTLIRNA	HSTLIRNA Human inter	197	82.8	17.7	12665	6	AK193632
125	110.2	23.5	717	6	I42449	I42449 Sequence	198	82.8	17.7	12665	6	AR542767
126	110.2	23.5	777	6	CS047661	CS047661 Sequence	199	82.8	17.7	12665	6	AC024704
127	110.2	23.5	777	8	AF031434	AF031434 Homo sapi	200	82.8	17.7	12665	6	AF067267
128	110.2	23.5	1684	8	HSTLIRNA	HSTLIRNA Human inter	201	82.8	17.7	12665	6	AR487066
129	110.2	23.5	1740	6	CQ861652	CQ861652 Sequence	202	82.8	17.7	12665	6	AR493824
130	110.2	23.5	1740	8	CS047655	CS047655 Sequence	203	82.8	17.7	12665	6	AK193630
131	110.2	23.5	1742	6	CS047655	CS047655 Sequence	204	82.8	17.7	12665	6	AC111146
132	110.2	23.5	1802	6	CS033142	CS033142 Sequence	205	82.8	17.7	12665	6	AC024704
133	110.2	23.5	1802	6	CS02094	CS02094 Sequence	206	82.4	17.6	12665	6	AF067267
134	110.2	23.5	1802	6	CS047662	CS047662 Sequence	207	74.6	15.9	92799	14	AC135817
135	110.2	23.5	1927	6	AX281640	AX281640 Sequence	208	71.2	15.0	6350	6	BD087375
136	110.2	23.5	1973	8	CS18896	CS18896 Sequence	209	71.2	15.2	6350	6	ES5194
137	110.2	23.5	2148	8	BC068441	BC068441 Homo sapi	210	71.2	15.2	6350	9	AC053920
138	110.2	23.5	459	6	AX200836	AX200836 Sequence	211	71.2	15.2	6350	9	AC024704
139	110.2	23.5	1366	6	AR204386	AR204386 Sequence	212	71.2	15.2	166465	9	L32838
140	109.2	23.3	1366	6	AR204387	AR204387 Sequence	213	71.2	15.2	177531	14	AC099634
141	109.2	23.3	1366	6	AR207389	AR207389 Sequence	214	70.2	15.0	5445	6	AC048817
142	109.2	23.3	1366	6	AR207390	AR207390 Sequence	215	70.2	15.0	5445	6	AC048818
143	109.2	23.3	1366	6	AX048814	AX048814 Sequence	216	70.2	15.0	5445	8	AF334756
144	109.2	23.3	1366	6	AX048816	AX048816 Sequence	217	70.2	15.0	7660	6	AFX594195
145	109.2	23.3	1376	6	AF334755	AF334755 Homo sapi	218	70.2	15.0	11129	8	AY972854
146	109.2	23.3	1707	8	BC009745	BC009745 Homo sapi	219	65.4	14.2	215	6	AC135817
147	108.6	23.2	1716	6	CQ981297	CQ981297 Sequence	220	64.6	13.8	4388	6	BD224186
148	108.6	23.2	1693	4	AB032628	AB032628 Sequence	221	64.6	13.8	4388	6	AR048818
149	108.6	22.0	339	6	AX206834	AX206834 Sequence	222	64.6	13.8	13017	6	AX167182
150	97.6	20.9	1036	4	AY026462	AY026462 Canis fam	223	60.8	13.0	472	6	CQ722803
151	97.6	20.5	563	6	AF216526	AF216526 Canis fam	224	60.8	13.0	474	6	BD077406
152	95.8	20.5	1594	4	RABTIRNA	RABTIRNA Rabbit inter	225	60.8	13.0	474	6	AR04389
153	95.8	20.5	1612	4	RABTIRNA	RABTIRNA Rabbit inter	226	60.8	13.0	477	6	AR048818
154	95.6	20.4	222	6	CS047651	CS047651 Sequence	227	60.8	13.0	477	6	AX048818
155	95.6	20.4	1614	6	AX172724	AX172724 Sequence	228	60.8	13.0	477	6	AX167182
156	95.6	20.4	321	6	CS047649	CS047649 Sequence	229	60.8	13.0	477	6	AR229782
157	95.4	20.4	603	6	AX127225	AX127225 Sequence	230	60.8	13.0	477	6	CO22803
158	95.4	20.4	1590	4	D83714	D83714 Equus cabal	231	56.6	12.1	764	10	BD224186
159	95.4	20.4	1590	6	BT019665	BT019665 Synthetic	232	54.2	11.6	562	5	CR90593
160	95.4	20.4	1614	6	BCU9482	BCU9482 Equus cabal	233	52.8	11.3	629	6	AX193643
161	95.4	20.4	1614	6	AX172724	AX172724 Sequence	234	52.8	11.3	520	6	AX193587
162	95.4	20.3	167423	14	AC145359	AC145359 Macropus	235	52.8	11.3	563	6	CQ722804
163	95.2	20.3	167423	14	AC145359	AC145359 Macropus	236	52.8	11.3	585	6	AR505137
164	95.2	20.3	167423	14	AC1453674	AC1453674 Sequence	237	52.8	11.3	585	6	AX052581

ALIGNMENTS

RESULT 1
 BD124061 BD124061 468 bp DNA
 LOCUS BD124061 polypeptide of IL-1-delta.
 DEFINITION BD124061
 ACCESSION BD124061

RESULT 2
BD263573
LOCUS BD263573
DEFINITION II-1 related polypeptides.
ACCESSION 468 bp
MATERIAL DNA
METHOD linear
DATE PAT 17-JUL-2003

ACCESSION	BD263573	DEFINITION	Homo sapiens interleukin-1 delta mRNA, complete cds.
VERSION	BD263573.1	ACCesion	AF230377
KEYWORDS	JP	VERsion	AF230377.1
SOURCE	JP	KEYWORDS	GI:9651788
ORGANISM	Homo sapiens (human)	SOURCE	Homo sapiens (human)
COMMENT		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
OS	Homo sapiens (human)	COMMENT	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
PD	JP 2002533122-A/7	REFERENCE	1 (bases 1 to 468)
PP	08-OCT-2002	AUTHORS	Goddard, A. and Pan, J.
PR	22-DEC-1995	TITLE	IL-1 related polypeptides
PP	JP 2000591188	JOURNAL	PATENT: JP 2002533122-A 2.08-OCT-2002;.
PR	13-APR-1999	GENEtech INC.	
PI	60/113430, 22-JAN-1999 US	OS	
PC	60/116843 PR	OS	
C12N5/10,		PD	JP 2002533122-A/7 08-OCT-2002.
CC	C12P21/02, C12P21/08, C12N15/00, C12N1/21, C12N1/19, C12N1/21, C12N5/00	PP	
CC	C12P21/02, C12P21/08, C12N15/00, C12N5/00	PR	
FT	IL-1 related polypeptides	PR	
FT	Key	PR	
FT	source	PR	
FT	1. .468	PR	
FEATURES	location/Qualifiers	PR	
source	/organism="Homo sapiens"	PR	
ORIGIN		PR	
Query Match	100.0%; Score 468; DB 6; Length 468;	PR	
Best Local Similarity	100.0%; Pred. No. 1. 9e-107;	PR	
Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PR	
Qy	1 ATGGTCTCTGAGTGGGGCGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Db	1 ATGGTCTCTGAGTGGGGCGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Qy	61 CTGGTAAATACCACTCTTGTAGCTGAGGCTGTCATGCGAGGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Db	61 CTGGTAAATACCACTCTTGTAGCTGAGGCTGTCATGCGAGGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Qy	61 CTGGTAAATACCACTCTTGTAGCTGAGGCTGTCATGCGAGGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Db	61 CTGGTAAATACCACTCTTGTAGCTGAGGCTGTCATGCGAGGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Qy	121 GAGATCAGGGTGGCCAAATCGGTGGCTGAGTGCAGCGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Db	121 GAGATCAGGGTGGCCAAATCGGTGGCTGAGTGCAGCGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Qy	181 GTCCAGGGTGGACGCGAGTGCCTGTCATGCGGGGGGAGGAGCCACTCTAACACTA	PR	
Db	181 GTCCAGGGTGGACGCGAGTGCCTGTCATGCGGGGGGAGGAGCCACTCTAACACTA	PR	
Qy	181 GTCCAGGGTGGACGCGAGTGCCTGTCATGCGGGGGGAGGAGCCACTCTAACACTA	PR	
Db	181 GTCCAGGGTGGACGCGAGTGCCTGTCATGCGGGGGGAGGAGCCACTCTAACACTA	PR	
Qy	241 GAGGCCAGTCACATCATGGAGCTTATCTGGTGGCTGAGTGCAGCGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Db	241 GAGGCCAGTCACATCATGGAGCTTATCTGGTGGCTGAGTGCAGCGCTGTCCTCCGAAATGAGGACTCGGCGATGGAGCTTAT	PR	
Qy	301 TACCGCGGGGACATGGGCTTACCTCCAGCTTGCAGTCAGTGCAGCGCTGTCCTACCGGGCTGGTC	PR	
Db	301 TACCGCGGGGACATGGGCTTACCTCCAGCTTGCAGTCAGTGCAGCGCTGTCCTACCGGGCTGGTC	PR	
Qy	301 TACCGCGGGGACATGGGCTTACCTCCAGCTTGCAGTCAGTGCAGCGCTGTCCTACCGGGCTGGTC	PR	
Db	301 TACCGCGGGGACATGGGCTTACCTCCAGCTTGCAGTCAGTGCAGCGCTGTCCTACCGGGCTGGTC	PR	
Qy	361 CTGTCACGGTGCCTGAGCGATCAGCTCAGACTCACCCAGCTTCCGAGATGT	PR	
Db	361 CTGTCACGGTGCCTGAGCGATCAGCTCAGACTCACCCAGCTTCCGAGATGT	PR	
Qy	421 GGCTGGAATGCCCAATCAGAAGCTCTACTTCCAGCAGTGTGACTAG	PR	
Db	421 GGCTGGAATGCCCAATCAGAAGCTCTACTTCCAGCAGTGTGACTAG	PR	
Qy	421 GGCTGGAATGCCCAATCAGAAGCTCTACTTCCAGCAGTGTGACTAG	PR	
Db	421 GGCTGGAATGCCCAATCAGAAGCTCTACTTCCAGCAGTGTGACTAG	PR	
RESULT	3	Db	361 CTGTCACGGTGCCTGAGCGATCAGCTCAGACTCACCCAGCTTCCGAGATGT
AP230377	420	Db	361 CTGTCACGGTGCCTGAGCGATCAGCTCAGACTCACCCAGCTTCCGAGATGT

QY	421	GGCTGGAATGCCCATCACAGACTCTACTTCCAGCAGTGACTAG	468	Db	61	CTGATATAAACAGCTCTAGCTGGAGCTGCAAGGAAGGTATAAAGGTGA	120
Db	421	GGCTGGAATGCCCATCACAGACTCTACTTCCAGCAGTGACTAG	468	Db	121	GAGATCAGCCTGCTTCAATCGGCTGCTGATGCCAGCTGTCCTCGGT	180
DEFINITION	AY890616	Synthetic construct Homo sapiens clone FLH141295.01X interleukin-1	468	Db	121	GAGATCAGCCTGCTTCAATCGGCTGCTGATGCCAGCTGTCCTCGGT	180
ACCESSION	AV890616	family member 5 (IL1F5) mRNA, complete cds.	468	Db	181	GTCCAGGGTGAAGCAGTCCTGCTGATGCCAGCTGTCCTCGGT	240
VERSION	AV890616.1	GI: 61364535	468	Db	241	GAGCAGTGACATCTGGAGCTCTATCTTGTGTCAGTGGGGAGGCGACTCTACCTC	300
KEYWORDS	Human ORF Project.			Db	301	TACCGCGACATCGGCTCACCTCCAGTCAAGAACATCCAGCTTCAAC	360
ORGANISM	Synthetic construct			Db	301	TACCGCGACATCGGCTCACCTCCAGTCAAGAACATCCAGCTTCAAC	360
REFERENCE	1 (bases 1 to 468)	other sequences; artificial sequences.		QY	361	CTGTCACGGCTGCTGAAGCGATCAGCTCAACCGAGCTCCGAGATGGT	420
AUTHORS	Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,P.,			Db	361	CTGTCACGGCTGCTGAAGCGATCAGCTCAACCGAGCTCCGAGATGGT	420
TITLE	Shen,B., Hallick,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,			Db	361	CTGTCACGGCTGCTGAAGCGATCAGCTCAACCGAGCTCCGAGATGGT	420
JOURNAL	Williamson,J. and LaBeer,J.	Cloning of human full-length CDS in Creator (TM) recombinational vector system		QY	421	GGCTGGAATGCCCATCACAGACTCTACTTCCAGCAGTGACTAG	468
REFERENCE	Unpublished			Db	421	GGCTGGAATGCCCATCACAGACTCTACTTCCAGCAGTGACTAG	468
AUTHORS	2 (bases 1 to 468)						
TITLE	Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,P.,						
JOURNAL	Shen,B., Hallick,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,						
COMMENT	Williamson,J. and LaBeer,J.						
Direct Submission (04-JAN-2005)	Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA						
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the Sall and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and 'GTC' before 'ATG' to provide Kozak consensus sequence-verified. Closely isolated and full-length sequence-verified.							
FEATURES	source	Location/Qualifiers					
	1. .468						
	/organism="Synthetic construct"						
	/mol_type="mRNA"						
	/db_xref="taxon:2630"						
	/clone="FLH141295.01X"						
	/lab_host="Escherichia coli DH5alpha T1 resistant"						
	/note="derived from MGC template"						
	1. .468						
	/gene="IL1F5"						
	1. .468						
	/gene="IL1F5"						
	/note="derived from MGC template"						
	1. .468						
	/transl_table=11						
	/product="interleukin 1 family member 5"						
	/db_xref="GI: 61364536"						
	/translaton="MVSAGLCPRMKOSALKVLYLHNOLLAGGLHAGKVKGELSV						
	VERMWLDSISPVNLVYGGSCGCGTCCGGCGTCAAGTCTTAAAGGTGAA						
	177						
	RDGLTSSFESAYPGWLCTVPEADQPVRLQDOPENGWNAPITDYFQODD"						
	ORIGIN						
	Query Match	100.0%; Score 468; DB 11; Length 468;					
	Best Local Similarity	100.0%; Pred. No. 1, 8e-107;					
	Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	58	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTTAT	117
Db	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	61	CTGCTATATACCACTCTAGCTGAGGACTCGGCTGTGAGGCTTAT	120
QY	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	118	CTGCTATATACCACTCTAGCTGAGGACTCGGCTGTGAGGCTTAT	177
Db	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	121	GAGATCAGCCTGCTCCAACTCGGTGGCTGATGCCAGCTGTCCTCGGT	180
QY	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	121	GAGATCAGCCTGCTCCAACTCGGTGGCTGATGCCAGCTGTCCTCGGT	180
Db	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	178	GAGATCAGCCTGCTCCAACTCGGTGGCTGATGCCAGCTGTCCTCGGT	237
QY	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	181	GTCCAGGGTGAAGCAGTCCTGCTGATGCCAGCTGTCCTCGGT	240
Db	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	238	GTCCAGGGTGAAGCAGTCCTGCTGATGCCAGCTGTCCTCGGT	297
QY	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	241	GAGCAGTGACATCATGGCTGTCTGCTGAGGACTCGGCTGTGAGGCTT	300
Db	1	ATGGTCTGAGGGGGCTGTCTCCGATGAGGACTCGGCTGTGAGGCTTAT	60	Db	298	GAGCAGTGACATCATGGCTGTCTGCTGAGGACTCGGCTGTGAGGCTT	357
QY	61	CTGCTATATACCACTCTAGCTGAGGACTCGGCTGTGAGGCTTAT	120	QY	301	TACCGGGGACATGGGCTCACCTCACCTCGAGTCGCTGCTGCTA	360

RESULT 6

Db 358 TACCGGGCGGGAATGGGACTCACTCCAGCTTGAGTCGGCTGCTACCCGAGCTCCCGAGATGTC 417

Qy 361 CTGTGCACCGTGCCTGAGAAGCCGATCAGCTGTCAGACTCACCCAGCTCCCGAGATGTC 420

Db 418 CTGTGCACCGTGCCTGAGAAGCCGATCAGCTGTCAGACTCACCCAGCTCCCGAGATGTC 477

Qy 421 GGCCTGGAATGCCCATACAGACTTCTACTTCAGCAGTGACTAG 468

Db 421 GGCCTGGAATGCCCATACAGACTTCTACTTCAGCAGTGACTAG 468

Qy 478 GGCCTGGAATGCCCATACAGACTTCTACTTCAGCAGTGACTAG 525

RESULT 7

Db211434 BD211434

DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.

ACCESSION BD211434

VERSION BD211434.1

KEYWORDS JP 2002510492 A/3.

SOURCE

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

A novel interleukin-1 receptor antagonist and uses thereof

AUTHORS Ford,J. and Pace,A.

JOURNAL Patent: JP 2002510492-A 09-AUG-2001

COMMENT

1 (bases 1 to 1282)

1. Debers,J.-F., Timans,J.-C., Bazan,J.-F. and Kastelein,R.A.

Mammalian interleukin-1-delta and -epsilon. Their use in therapeutic and diagnostic methods

Patent: WO 015219-A 10-AUG-2001

JOURNAL SCHERING CORPORATION (US)

FEATURES

1. Location/Qualifiers

1. -1025

/organism="unidentified"

/mol_type="unassigned DNA"

/ab_xref="taxon:32644"

/note="Description of Unknown organism: primate; surmised Homo Sapiens"

58. - 525

/not_e="unnamed protein product"

/codon_start=1

/protein_id="CACC0372.1"

/ab_xref="GI:1522466"

/translation="MVSIGALCPRMKDOSALKVLYHNQNLLAGGIHAGKVVKGEITSVVPRWLDASLIVLNGTGGCGCFLRQSGCUCVQGOBTTLTLPVNIMELLYIYGAKVKSFTYR

RDMLGTSFPEASAYPGWFLCTVPEADOPVRLQLPENGWNAPITDYFQQCD"

ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1025;

Best Local Similarity 100.0%; Pred. No. 1 8e-107; Mismatches 0; Indels 0; Gaps 0;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGTGGGGCGCTGTGCTTCCGAAATGAGGACTCGGGATGAGGCTTAT 60

Db 58 ATGGTCTGAGTGGGGCGCTGTGCTTCCGAAATGAGGACTCGGGATGAGGCTTAT 117

Qy 61 CTGCTAAATACCAAGCTTCTAGCTGAGGGCTGATCGAGGGAAGGTCTTAAGGTAA 120

Db 118 CTGCTAAATACCAAGCTTCTAGCTGAGGGCTGATCGAGGGAAGGTCTTAAGGTAA 177

Qy 121 GAGATCAGGGTGGCCCATGCTGGCTGAGCTGAGGGAAGGTCTTAAGGTAA 180

Db 178 GAGATCAGGGTGGCCCATGCTGGCTGAGGGAAGGTCTTAAGGTAA 237

Qy 181 GTCCAGGGTGGAGCCAGTCAGCTGAGGGAAGGTCTTAAGGTAA 240

Db 238 GTCCAGGGTGGAGCCAGTCAGCTGAGGGAAGGTCTTAAGGTAA 297

Qy 241 GAGCCAGTGAACATCATGGAGGTCTATCTGGTSCCAAGGATCAAGAGCTTCACCTC 300

Db 298 GAGCCAGTGAACATCATGGAGGTCTATCTGGTSCCAAGGATCAAGAGCTTCACCTC 357

Qy 301 TACCGGGGCAATGGGTGACCTTGAGTCGCTGCTACCCGGGCTGGTTC 360

Db 358 TACCGGGGCAATGGGTGACCTTGAGTCGCTGCTACCCGGGCTGGTTC 417

Qy 361 CTGTGCAGGGTGCCTGAGAAGCCGATCAGCTGTCAGACTCACCCAGCTCCCGAGATGTC 420

Db 418 CTGTGCAGGGTGCCTGAGAAGCCGATCAGCTGTCAGACTCACCCAGCTCCCGAGATGTC 477

Qy 421 GGCCTGGAATGCCCATACAGACTTCTACTTCAGCAGTGACTAG 468

Db 478 GGCCTGGAATGCCCATACAGACTTCTACTTCAGCAGTGACTAG 525

RESULT 8

Db211434 BD211434

DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.

ACCESSION BD211434

VERSION BD211434.1

KEYWORDS JP 2002510492 A/3.

SOURCE

ORGANISM Homo sapiens (human)

Patent: JP 2002510492-A 3 09-APR-2002

HYSEQ INC

COMMENT Homo sapiens (human)

OS JP 2002510492-A/3

PN

FD 09-APR-2002

PP 05-APR-1999 JP 2000542457

PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR

20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR

31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR

17-FEB-1999 US 09/251370

PI JOHN FORD, ANNE PACE

PC C12N15/09, A61K37/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15, C12N1/21, C12N5/10, C12Q1/68, G01N33/50, G01N33/566, G01N33/68, PC

PC C12N15/00, A61K37/02, C12N5/00

CC A novel interleukin-1 receptor antagonist and uses thereof

Key

FT source

FT 1. -1282

/organism="Homo sapiens (human)".

FEATURES

source

1. -1282

/organism="Homo sapiens"

/mol_type="genomic DNA"

/ab_xref="taxon:96061"

ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;

Best Local Similarity 100.0%; Pred. No. 1 8e-107; Mismatches 0; Indels 0; Gaps 0;

Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGTGGGGCGCTGTGCTTCCGAAATGAGGACTCGGGATGAGGCTTAT 60

Db 73 ATGGTCTGAGTGGGGCGCTGTGCTTCCGAAATGAGGACTCGGGATGAGGCTTAT 132

Qy 61 CTGCTAAATACCAAGCTTCTAGCTGAGGGCTGATCGAGGGAAGGTCTTAAGGTAA 120

Db 133 CTGCTAAATACCAAGCTTCTAGCTGAGGGCTGATCGAGGGAAGGTCTTAAGGTAA 192

Qy 121 GAGATCAGGGTGGCCCATGCTGGCTGAGCTGAGGGAAGGTCTTAAGGTAA 180

Db 193 GAGATCAGGGTGGCCCATGCTGGCTGAGGGAAGGTCTTAAGGTAA 252

Qy 181 GTCCAGGGTGGAGCCAGTCAGCTGAGGGAAGGTCTTAAGGTAA 240

Db 253 GTCCAGGGTGGAGCCAGTCAGCTGAGGGAAGGTCTTAAGGTAA 312

Qy 241 GAGCCAGTGAACATCATGGAGGTCTATCTGGTSCCAAGGATCAAGAGCTTCACCTC 300

FEATURES	Location/Qualifiers
source	Location/Qualifiers
	1. .1282
	/organism="unknown"
	/mol_type="genomic DNA"
ORIGIN	ORIGIN
	Query Match 100.0%; Score 468; DB 6; Length 1282;
	Best Local Similarity 100.0%; Pred. No. 1. 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	OY
1	ATGTCCTCGAGTGGCGCTGCTGCTCCGAAATGAGGAGCTGCGCATGAGGCTTAT 60
Db	Db
73	ATGGTCCTCGAGTGGCGCTGCTGCTCCGAAATGAGGAGCTGCGCATGAGGCTTAT 132
OY	OY
61	CTGCATAATACCGCTCTAGTGGAGGCTCATGAGGAGCTTAT 132
Qy	Qy
61	CTGCATAATACCGCTCTAGTGGAGGCTCATGAGGAGCTTAT 120
Db	Db
133	CTGCATAATACCGCTCTAGTGGAGGCTCATGAGGAGCTTAT 192
OY	OY
121	GAGATCAGGGTGGCCCATGGTGGCTGAGATCCAGCTGGTGGCTGCTGGT 180
Qy	Qy
193	GAGATCAGGGTGGCCCATGGTGGCTGAGATCCAGCTGGTGGCTGCTGGT 252
Db	Db
181	GTCCAGGGTGGAGCCAGTGCCTCATGAGGAGCTTACACTA 240
Db	Db
253	GTCCAGGGTGGAGCCAGTGCCTCATGAGGAGCTTACACTA 312
Qy	Qy
241	GASCCAGTGAACTCATGCTGAGCTATCTGTGGTCCGAGGATCAGCTTCACCTTC 300
Db	Db
313	GAGCCAGTGAACTCATGCTGAGCTATCTGTGGTCCGAGGATCAGCTTCACCTTC 372
OY	OY
301	TACCGGGGGACATGGGGTCACTCCAGCTCGAGTGGCTACCGGCTGGTTC 360
Db	Db
373	TACCGGGGGACATGGGGTCACTCCAGCTCGAGTGGCTACCGGCTGGTTC 432
OY	OY
361	CTGTCGACCGTGTGCTGAAGCCGATCAGCTGAGCTACCCAGCTTCCGAGAATGTT 420
Db	Db
433	CTGTCGACCGTGTGCTGAAGCCGATCAGCTGAGCTTCCAGCAGTGTGACTAG 540
OY	OY
421	GGCTGGAATGCCCATACAGACTCTACTCCAGACTGTGACTAG 468
Db	Db
493	GGCTGGAATGCCCATACAGACTCTACTCCAGCAGTGTGACTAG 492
RESULT 11	RESULT 11
AX069307	AX069307
LOCUS	1282 bp
DEFINITION	DNA
VERSION	1
ACCESSION	GI:12579179
KEYWORDS	
ORGANISM	
REFERENCE	
AUTHORS	Ford, J. and Pace, A.
TITLE	A interleukin-1 receptor antagonist and uses thereof
JOURNAL	Patent: WO 0125711-A 4 11-JAN-2001; HYSEQ, INC. (US)
FEATURES	Location/Qualifiers
source	1. .1282
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
	/note="unnamed protein product"
CDS	CDS
	/codon_start=1
	/protein_id="CAC27298_1"
	/db_xref="GI:12579180"
	(translation="MVLSGALCFRMKDSALKVILYHNNOLLAGLHAGKVKGIEISV
	PRWRWLDLSPLSPVILVGVOGGSQCLSCGVOQEPIITLSEVNIMELYLAKESKSFPTFR
	RDWGLTSSFPESAAYPGWFLCTVPEADQPVRLTQLEPENGQWNAPI TDYFQOCD"
RESULT 12	RESULT 12
AF201894	AF201894
LOCUS	1288 bp
DEFINITION	mRNA
VERSION	1
ACCESSION	AF201894
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthozia; Euarchoptilires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	
AUTHORS	Smith, D.E., Renshaw, B.R., Ketcham, R.R., Kubin, M., Garka, K.E. and Sims, J.E.
TITLE	Four new members expand the interleukin-1 superfamily
JOURNAL	J. Biol. Chem. 275(2), 1169-1175 (2000)
PUBMED	10625660
REFERENCE	
AUTHORS	2 (bases 1 to 1288)
TITLE	Submitted (04-Nov-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
JOURNAL	Location/Qualifiers
FEATURES	1. .1288
source	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/chromosome="2"
	/map="2q; between D2S121 and D2S110"
	28 .495
	/note="Similar to IL-1"
	/codon_start=1
	/product="fill delta"

ORIGIN	<pre> /protein_id="NAFP5210.1" /db_xref="GI:694388" /translation="MVLVQALPFRMKDOSALKVLYHNNOLLAGGVLHAGKVTKGEISV VNRLWDLASLSPVILQVQGSQCLISCGVQETLTLBPNVNLMLYLAKESEKSFV RDMLTSSPESAVYPGWPLCTVPEADOPVRLQLPENGWNAPITDFYFQOD" </pre>	
Query Match	100.0%; Score 468; DB 8; Length 1288;	Db
Best Local Similarity	100.0%; Pred. No. 1 8e-107;	Qy
Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db
FEATURES	<p>source 1. : 2563</p> <p>organism "Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>	
ORIGIN	<pre> Query Match 100.0%; Score 468; DB 6; Length 2598; Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </pre>	
Query Match	100.0%; Score 468; DB 6; Length 2563;	Qy
Best Local Similarity	100.0%; Pred. No. 1 8e-107;	Db
Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy
RESULT 13	<p>AX080389 AX080389 Sequence 1 from Patent WO0105974. 2563 bp DNA linear PAT 22-FEB-2001</p> <p>DEFINITION Sequence 1 from Patent WO0105974.</p> <p>ACCESSION AX080389</p> <p>VERSION AX080389.1 GI:13159840</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p>	
REFERENCE	<p>AUTHORS Eaton, D. L., Filvaroff, E., Gerritsen, M. E., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Watane, C. K. and Wood, W. I.</p> <p>TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same</p> <p>JOURNAL Patent: WO 0116318-A 151 08-MAR-2001;</p> <p>FEATURES source 1. : 2598</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>	
ORIGIN	<pre> Query Match 100.0%; Score 468; DB 6; Length 2598; Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </pre>	
FEATURES	<p>source 1. : 2563</p> <p>organism "Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>	
ORIGIN	<pre> Query Match 100.0%; Score 468; DB 6; Length 2598; Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </pre>	
ORIGIN	<pre> Query Match 61 CTGATAATACCACTCTAGCTGGAGGCTGATGAGGAAAGTCATTAAGGAA 120 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 61 CTGATAATACCACTCTAGCTGGAGGCTGATGAGGAAAGTCATTAAGGAA 120 </pre>	
ORIGIN	<pre> Query Match 150 GAGATCAGCTGGTCCCCTACGGTGGCTGATGCCAGCTGTC 209 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 150 GAGATCAGCTGGTCCCCTACGGTGGCTGATGCCAGCTGTC 209 </pre>	
ORIGIN	<pre> Query Match 181 GAGATCAGCTGGTCCCCTACGGTGGCTGATGCCAGCTGTC 207 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 181 GAGATCAGCTGGTCCCCTACGGTGGCTGATGCCAGCTGTC 207 </pre>	
ORIGIN	<pre> Query Match 210 GTCAGGGTGAAGCCAGCTCTAGCTGGAGGCGACTCTAACACTA 269 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 210 GTCAGGGTGAAGCCAGCTCTAGCTGGAGGCGACTCTAACACTA 269 </pre>	
ORIGIN	<pre> Query Match 241 GAGCCAGTGAACATCGAGCTCTATCTGTCGCAAGGATCCAGAGCTTACCTTC 300 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 241 GAGCCAGTGAACATCGAGCTCTATCTGTCGCAAGGATCCAGAGCTTACCTTC 300 </pre>	
ORIGIN	<pre> Query Match 270 GAGCCAGTGAACATCGAGCTCTATCTGTCGCAAGGATCCAGAGCTTACCTTC 329 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 270 GAGCCAGTGAACATCGAGCTCTATCTGTCGCAAGGATCCAGAGCTTACCTTC 329 </pre>	
ORIGIN	<pre> Query Match 301 TACCGGGGACATGGGGCTACCTCCAGCTTCAGTCGCTGCTGCTAACCGGGCTGGTC 360 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 301 TACCGGGGACATGGGGCTACCTCCAGCTTCAGTCGCTGCTGCTAACCGGGCTGGTC 360 </pre>	
ORIGIN	<pre> Query Match 328 TACCGGGGACATGGGGCTACCTCCAGCTTCAGTCGCTGCTGCTAACCGGGCTGGTC 387 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 328 TACCGGGGACATGGGGCTACCTCCAGCTTCAGTCGCTGCTGCTAACCGGGCTGGTC 387 </pre>	
ORIGIN	<pre> Query Match 361 CTGTCACGGTGCCTGAAAGCCGATCAGCTCAGCTCCGAGATGCT 420 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 361 CTGTCACGGTGCCTGAAAGCCGATCAGCTCAGCTCCGAGATGCT 420 </pre>	
ORIGIN	<pre> Query Match 388 CTGTCACGGTGCCTGAAAGCCGATCAGCTCAGCTCCGAGATGCT 447 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 388 CTGTCACGGTGCCTGAAAGCCGATCAGCTCAGCTCCGAGATGCT 447 </pre>	
ORIGIN	<pre> Query Match 421 GCTGGAATGCCCATCACAGACTCTACTCCAGCAGTGTGACTAG 468 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 421 GCTGGAATGCCCATCACAGACTCTACTCCAGCAGTGTGACTAG 468 </pre>	
ORIGIN	<pre> Query Match 449 GCTGGAATGCCCATCACAGACTCTACTCCAGCAGTGTGACTAG 495 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 449 GCTGGAATGCCCATCACAGACTCTACTCCAGCAGTGTGACTAG 495 </pre>	
RESULT 14	<p>AX092420 AX092420 Sequence 51 from Patent WO016318. 2598 bp DNA linear PAT 21-MAR-2001</p> <p>DEFINITION Sequence 51 from Patent WO016318.</p> <p>ACCESSION AX092420</p> <p>VERSION AX092420.1 GI:13444524</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p>	
REFERENCE	<p>AUTHORS Eaton, D. L., Filvaroff, E., Gerritsen, M. E., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Watane, C. K. and Wood, W. I.</p> <p>TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same</p> <p>JOURNAL Patent: WO 0116318-A 151 08-MAR-2001;</p> <p>FEATURES source 1. : 2598</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>	
ORIGIN	<pre> Query Match 61 CTGATAATACCACTCTAGCTGGAGGCTGATGAGGAAAGTCATTAAGGAA 120 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 61 CTGATAATACCACTCTAGCTGGAGGCTGATGAGGAAAGTCATTAAGGAA 120 </pre>	
ORIGIN	<pre> Query Match 127 CTGATAATACCACTCTAGCTGGAGGCTGATGAGGAAAGTCATTAAGGAA 186 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 127 CTGATAATACCACTCTAGCTGGAGGCTGATGAGGAAAGTCATTAAGGAA 186 </pre>	
ORIGIN	<pre> Query Match 121 GAGATCAGCTGGGGCCATCGCTGGATGCCACCTGTC 180 Best Local Similarity 100.0%; Pred. No. 1 8e-107; Matches 121 GAGATCAGCTGGGGCCATCGCTGGATGCCACCTGTC 180 </pre>	

Db 187 GAGATCAGGTGGTGGTCCCCATCGTGGCTGGATCCAGCTGCTGCTGCTGGGGGGGGGGAGGAGCCACTCTAACCTA 246
 Qy 181 GTCCAGGGGGAGCCAGCTGCTCTCATGCTGGGGGGAGGAGCTCTAACCTA 240
 Db 247 GTCCAGGGGGAGCCAGCTGCTCTCATGCTGGGGGGAGGAGCTCTAACCTA 306
 Qy 241 GAGCAGTGAACATCATGGAGCTCTGTCAGTGGCCAGGAACTCTAACCTA 306
 Db 307 GAGCAGTGAACATCATGGAGCTCTGTCAGTGGCCAGGAACTCTAACCTA 366
 Qy 301 TACCGGGGGAGCATGGGGCTACCTCCAGCTCTGAGCTGGCTACCGGACTCTAACCTC 360
 Db 367 TACCGGGGGAGCATGGGGCTACCTCCAGCTCTGAGCTGGCTACCGGACTCTAACCTC 426
 Qy 361 CTGTGCACTGGTGCCTGAGGCCGATCAGCTGTCAGACTCACCTGACCTCCAGCTGCTGAGCTTCCCGAGAATGTT 420
 Db 427 CTGTGCACTGGTGCCTGAGGCCGATCAGCTGTCAGACTCACCTCCAGCTTCCGAGAATGTT 486
 Qy 421 GGCCTGGAATGCCCATACAGACTCTACTCCAGCACTGTGACTAG 468
 Db 487 GGCCTGGAATGCCCATACAGACTCTACTCCAGCACTGTGACTAG 534

RESULT 15) AX454730
 LOCUS AX454730 2598 bp DNA linear PAT 06-JUL-2002
 DEFINITION Sequence 315 from Patent WO2008284.
 ACCESSION AX454730.1 GI:21713989
 VERSION 1
 KEYWORDS SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Bimkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE AUTHORS
 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillian, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watana, C.K., Williams, P.M., Wood, W.I. and Ye, W.
 TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
 Patent: WO 0208284-A 315 31-JAN-2002; Genentech, Inc. (US); Ferrara, Napoleone (US); Gerber, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillian, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watana, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)
 FEATURES source
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 100.0%; Score 468; DB 6; Length 2598; Best Local Similarity 100.0%; Pred. No. 1.8e-107; Mismatches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 468; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCTCTGAGGGGGGGCTCTGCTCCGATGAGGACTCGGATGAGGCTTAT 60
 Db 61 ATGGCTCTGAGGGGGGGCTCTGCTCCGATGAGGACTCGGATGAGGCTTAT 120
 Qy 61 ATGGCTCTGAGGGGGGGCTCTGCTCCGATGAGGACTCGGATGAGGCTTAT 126
 Db 67 ATGGCTCTGAGGGGGGGCTCTGCTCCGATGAGGACTCGGATGAGGCTTAT 186
 Qy 121 GAGATCAGCTGAGTGGGGGGCTCTGCTCCGATGAGGACTCGGATGAGGCTTAT 180
 Db 187 GAGATCAGCTGAGTGGGGGGCTCTGCTCCGATGAGGACTCGGATGAGGCTTAT 246
 Qy 181 GTCCAGGGGGAGCCAGCTGCTCTCATGCTGGGGGGAGGAGCTCTAACCTA 240
 Db 247 GTCCAGGGGGAGCCAGCTGCTCTCATGCTGGGGGGAGGAGCTCTAACCTA 306

QY 301 TACCGCCGGGACATGGGCTCACCTCAGCTCGAGTCGGCTACCCGGGTGGTC 360
 Db 367 TACCGGGGGACATGGGCTCACCTCAGCTCGAGTCGGCTACCCGGGTGGTC 426
 QY 361 CTGTCACGGCTGCTGAAGCGATCAGCCCTGAGACTCACCCAGCTCCGAGATGT 420
 Db 427 CTGTCACGGCTGCTGAAGCGATCAGCCCTGAGACTCACCCAGCTCCGAGATGT 486
 QY 421 GCCTGGAATGCCCTATCAGACTCTACTTCCAGACTGTGACTAG 468
 Db 487 GCCTGGAATGCCCTATCAGACTCTACTTCCAGACTGTGACTAG 534

RESULT 17
 LOCUS AY359117 2598 bp mRNA linear PRI 03-OCT-2003
 DEFINITION Homo sapiens clone DNA96787 IL1HY1 (UNQ1896) mRNA, complete cds
 ACCESSION AY359117
 VERSION AY359117.1 GI:3183350
 KEYWORDS F11C CNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo
 REFERENCE 1 (bases 1 to 2598)
 AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Curreli, B., Duei, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schonfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vaghe, A., Vandelli, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yanbara, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
 JOURNAL Genome Res., 13 (10), 2265-2270 (2003)
 PUBLMED 12575309
 REFERENCE 2 (bases 1 to 2598)
 AUTHORS Clark, H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 FEATURES source
 gene
 cds
 ORIGIN

Query Match Best Local Similarity 100.0%; Score 468; DB 8; Length 2598;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCTGGTGGGGCGCTGCTCCGATGAGGACTCGGATGAGGAGCTTAT 60
 Db 67 ATGAGCTCTGGTGGGGCGCTGCTCCGATGAGGACTCGGATGAGGAGCTTAT 126

RESULT 18
 LOCUS HSA242738 2604 bp mRNA linear PRI 15-APR-2005
 DEFINITION Homo sapiens mRNA for interleukin-1-like protein 1 (IL11 gene) transcript 2.
 ACCESSION AU242738
 VERSION AU242738.1 GI:6165335
 KEYWORDS IL11 gene, interleukin-1-like protein 1.
 SOURCE Homo sapiens (human)
 ORGANISM Butheria; Euarchontoglires; Primates; Catarrhini; Mammalia; Homo
 REFERENCE 1 (bases 1 to 2604)
 AUTHORS Barton, J.L., Herbst, R., Bosio, D., Higgins, L. and Nicklin, M.J.
 TITLE A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1 α , IL-1 β and IL-1 β antagonist activities
 JOURNAL Eur. J. Immunol. 30 (11), 3299-3308 (2000)
 PUBLMED 11091146
 REFERENCE 2 (bases 1 to 2604)
 AUTHORS Nicklin, M.J.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1999) Nicklin, M.J.: Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
 FEATURES source
 gene
 cds
 ORIGIN

Query Match Best Local Similarity 100.0%; Score 468; DB 8; Length 2598;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCTGGTGGGGCGCTGCTCCGATGAGGACTCGGATGAGGAGCTTAT 60
 Db 67 ATGAGCTCTGGTGGGGCGCTGCTCCGATGAGGACTCGGATGAGGAGCTTAT 126

RESULT 19
 LOCUS 301 TACCGGGGACATGGGCTCACCTCAGCTCGAGTCGGCTACCCGGGTGGTC 360
 DEFINITION Homo sapiens mRNA for interleukin-1-like protein 1 (IL11 gene) transcript 1.
 ACCESSION 367 TACCGGGGACATGGGCTCACCTCAGCTCGAGTCGGCTACCCGGGTGGTC 426
 VERSION 361 CTGTCACGGCTGCTGAAGCGATCAGCCCTGAGACTCACCCAGCTCCGAGATGT 420
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo
 REFERENCE 1 (bases 1 to 2604)
 AUTHORS Barton, J.L., Herbst, R., Bosio, D., Higgins, L. and Nicklin, M.J.
 TITLE A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1 α , IL-1 β and IL-1 β antagonist activities
 JOURNAL Eur. J. Immunol. 30 (11), 3299-3308 (2000)
 PUBLMED 11091146
 REFERENCE 2 (bases 1 to 2604)
 AUTHORS Nicklin, M.J.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1999) Nicklin, M.J.: Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
 FEATURES source
 gene
 cds
 ORIGIN

Query Match Best Local Similarity 100.0%; Score 468; DB 8; Length 2598;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCTGGTGGGGCGCTGCTCCGATGAGGACTCGGATGAGGAGCTTAT 60
 Db 67 ATGAGCTCTGGTGGGGCGCTGCTCCGATGAGGACTCGGATGAGGAGCTTAT 126

ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 2604;
Best Local Similarity 100.0%; Pred. No. 1. 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 ATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAGGACTCTGGCATGAGGACTT 60
Db 73 ATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAGGACTCTGGCATGAGGACTT 132
Ov 61 CTGCGATAATACCAAGCTTCTAGCTGAGGCGCTCATGAGGAGGCTTAAAGGTAA 120
Db 133 CTGCGATAATACCAAGCTTCTAGCTGAGGCGCTCATGAGGAGGCTTAAAGGTAA 192
Ov 121 GAGATCAGGGTGGTCCCATTGGTGCCTGGATCCAGGCTGTCCTGGCTATCTGGT 180
Db 193 GAGATCAGGGTGGTCCCATTGGTGCCTGGATCCAGGCTGTCCTGGT 252
Ov 181 GTCCAGGGTGGAAAGCCAGTGCCTCATGAGGAGGCTTAAAGGTAA 240
Db 253 GTCCAGGGTGGAAAGCCAGTGCCTCATGAGGAGGCTTAAAGGTAA 312
Ov 241 GAGCCAGTGAAATCATGAGCTCATGGAGCTCTATCTGTCGCAAGGATCAAGCTTACCTTC 300
Db 313 GAGCCAGTGAAATCATGAGCTCATGGAGCTCTATCTGTCGCAAGGATCAAGCTTACCTTC 372
Ov 301 TACCGGGGAGCATGGGTCACTCCAGCTCGAGTCGGCTCTACCGGCTGGTC 360
Db 373 TACCGGGGAGCATGGGTCACTCCAGCTCGAGTCGGCTCTACCGGCTGGTC 432
Ov 361 CTGCGACCGGTGCCTGAAGCCGATCGCCTGTCAGACTCACCCAGCTTCCCGAATGGT 420
Db 433 CTGCGACCGGTGCCTGAAGCCGATCGCCTGTCAGACTCACCCAGCTTCCCGAATGGT 492
Ov 421 GCGTGGATGCCCATCACAGACTCTACTCTCAGACTGTGACTAG 468
Db 493 GCGTGGATGCCCATCACAGACTCTACTCTCAGACTGTGACTAG 540

RESULT 19

HS242737 HSA242737 2613 bp mRNA for interleukin-1-like protein-1 (IL1L gene), linear PRI 15-APR-2005
LOCUS Homo sapiens mRNA for interleukin-1-like protein-1 (IL1L gene),
DEFINITION transcript 1.
ACCESSION AJ242737
VERSION AJ242737.1
KEYWORDS GI:6165333
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Burchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Barton,J.L., Herbst,R., Bosio,D., Higgins,L. and Nicklin,M.J.
TITLE A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
JOURNAL Eur. J. Immunol. 30 (11), 3299-3308 (2000)
PUBLISHED 11/09/2006
REFERENCE 2 (bases 1 to 2613)
AUTHORS Nicklin,M.J.
TITLE Direct submission
JOURNAL Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire

ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 2613;
Best Local Similarity 100.0%; Pred. No. 1. 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 ATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAGGACTCTGGCATGAGGACTT 60
Db 82 ATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAGGACTCTGGCATGAGGACTT 141
Ov 61 CTGCGATAATACCAAGCTTCTAGCTGAGGCGCTCATGAGGAGGCTTAAAGGTAA 120
Db 142 CTGCGATAATACCAAGCTTCTAGCTGAGGCGCTCATGAGGAGGCTTAAAGGTAA 201
Ov 121 GAGATCAGGGTGGTCCCATTGGTGCCTGGATCCAGGCTGTCCTGGCTATCTGGT 180
Db 202 GAGATCAGGGTGGTCCCATTGGTGCCTGGATCCAGGCTGTCCTGGCTATCTGGT 261
Ov 181 GTCCAGGGTGGAAAGCCAGTGCCTGTCAGTGGGGTGGGGCTGGAGGAGCCACTTACACTA 240
Db 262 GTCCAGGGTGGAAAGCCAGTGCCTGTCAGTGGGGTGGGGCTGGAGGAGCCACTTACACTA 321
Ov 241 GAGCCAGTGAAATCATGAGCTCATGGAGCTTACCTCTGTCAGACTGGCTGGAGGAGGCTTACCTTC 300
Db 322 GAGCCAGTGAAATCATGAGCTCATGGAGCTTACCTCTGTCAGACTGGCTGGAGGAGGCTTACCTTC 381
Ov 301 TACCGGGGAGCATGGGTCACTCCAGCTGTCAGTGGCTGGAGGAGGCTTACCCGGCTGGT 360
Db 382 TACCGGGGAGCATGGGTCACTCCAGCTGTCAGTGGCTGGAGGAGGCTTACCCGGCTGGT 441
Ov 361 CTGCGACGGTGCCTGAAGCCGATCGCCTGTCAGACTCACCCAGCTTCCCGAGATGGT 420
Db 442 CTGCGACGGTGCCTGAAGCCGATCGCCTGTCAGACTCACCCAGCTTCCCGAGATGGT 501
Ov 421 GCGTGGATGCCCATCACAGACTCTACTCTCAGACTGTGACTAG 468
Db 502 GCGTGGATGCCCATCACAGACTCTACTCTCAGACTGTGACTAG 549

RESULT 20

BD211435

FEATURES

Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
source
1. .2613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2q11-13"
/tissue_type="Placenta"
/note="Between IL1B and IL1RN"
1. .2613
/gene="IL1L"
/gene="IL1L"
/gene="IL1L"
/functions="putative cytokine"
/codon_start=1
/product="interleukin-1-like protein-1"
/protein_id="CAB59322.1"
/ab_xref="UniProt:Q9UBH0"
/ab_xref="GOA:Q9UBH0"
/ab_xref="InterPro:IPR009975"
/ab_xref="InterPro:IPR03296"
/ab_xref="InterPro:IPR03297"
/ab_xref="UniProt:IPR008996"
/translation="MVLISGALCFRNUSAKLYINNQIAGLHLAKVVKGERISV
VNRWIDASISSPVILGVQGGSQCLSGVQGQBLPTLEPVNIMELVIGAKESKSFFYR
RDMGLTSSFESAYPGWFLCTVPEADQPVRLTOLPENGWNNAPITDVFYFQOCD"
/gene="IL1L"
/citations=11
/evidence=experimental

ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 2613;
Best Local Similarity 100.0%; Pred. No. 1. 8e-107; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 ATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAGGACTCTGGCATGAGGACTT 60
Db 82 ATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAGGACTCTGGCATGAGGACTT 141
Ov 61 CTGCGATAATACCAAGCTTCTAGCTGAGGCGCTCATGAGGAGGCTTAAAGGTAA 120
Db 142 CTGCGATAATACCAAGCTTCTAGCTGAGGCGCTCATGAGGAGGCTTAAAGGTAA 201
Ov 121 GAGATCAGGGTGGTCCCATTGGTGCCTGGATCCAGGCTGTCCTGGCTATCTGGT 180
Db 202 GAGATCAGGGTGGTCCCATTGGTGCCTGGATCCAGGCTGTCCTGGCTATCTGGT 261
Ov 181 GTCCAGGGTGGAAAGCCAGTGCCTGTCAGTGGGGTGGGGCTGGAGGAGCCACTTACACTA 240
Db 262 GTCCAGGGTGGAAAGCCAGTGCCTGTCAGTGGGGTGGGGCTGGAGGAGCCACTTACACTA 321
Ov 241 GAGCCAGTGAAATCATGAGCTCATGGAGCTTACCTCTGTCAGACTGGCTGGAGGAGGCTTACCTTC 300
Db 322 GAGCCAGTGAAATCATGAGCTCATGGAGCTTACCTCTGTCAGACTGGCTGGAGGAGGCTTACCTTC 381
Ov 301 TACCGGGGAGCATGGGTCACTCCAGCTGTCAGTGGCTGGAGGAGGCTTACCCGGCTGGT 360
Db 382 TACCGGGGAGCATGGGTCACTCCAGCTGTCAGTGGCTGGAGGAGGCTTACCCGGCTGGT 441
Ov 361 CTGCGACGGTGCCTGAAGCCGATCGCCTGTCAGACTCACCCAGCTTCCCGAGATGGT 420
Db 442 CTGCGACGGTGCCTGAAGCCGATCGCCTGTCAGACTCACCCAGCTTCCCGAGATGGT 501
Ov 421 GCGTGGATGCCCATCACAGACTCTACTCTCAGACTGTGACTAG 468
Db 502 GCGTGGATGCCCATCACAGACTCTACTCTCAGACTGTGACTAG 549

Locus BD211435 2648 bp DNA linear PAT 17-JUN-2003
 Definition A novel interleukin-1 receptor antagonist and uses thereof.
 Accession BD211435
 Version BD211435.1 GI:33021205
 Keywords
 Source Homo sapiens
 Organism Homo sapiens
 Burkhardt; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchoptoglires; Primates; Catarrhini;
 Homidae; Homo
 Reference 1 (bases 1 to 2648)
 Authors Ford,J. and Pace,A.
 Title A novel interleukin-1 receptor antagonist and uses thereof
 Journal Patent: JP 2002510492-A 4 09-APR-2002;
 Comment HYSEQ INC
 OS Homo sapiens (human)
 PN JP 2002510492-A/4
 PD 09-APR-2002
 PF 05-APR-1999 JP 2000542457
 PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
 20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
 31-JUL-1998 US 09/121768,13-JAN-1999 US 09/229591 PR
 17-FEB-1999 US 09/251370
 PI JOHN FORD ANN PACE
 PC C12N15/09,A61K39/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,
 PC C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/566,G01N33/68, PC
 PC A61K3//02,C12N5/00
 CC A novel interleukin-1 receptor antagonist and uses thereof PH
 Key
 FT source Location/Qualifiers 1. . 2648
 FT source Location/Qualifiers 1. . 2648
 FEATURES source /organism="Homo sapiens" .
 ORIGIN
 Query Match 100.0%; Score 468; DB 6; Length 2648;
 Best Local Similarity 100.0%; Pred. No. 1.8e-17;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Ov 1 ATGGTCTCTAGTGGGGCGCTGTCCTCCATAGAGGACTCGGCATGGAGGCTTAT 60
 Db 62 ATGGTCTCTAGTGGGGCGCTGTCCTCCATAGAGGACTCGGCATTAGGCTTAT 121
 Ov 61 CTGCATAATACCGCTCTAGCTGGAGGGCTGATGCCAGGCTGCCCCGGTCTCTGGT 120
 Db 122 CTGCATAATACCGCTCTAGCTGGAGGGCTGATGCCAGGCTGCCCCGGTCTCTGGT 181
 Ov 121 GAGATCAGGGGTOCCAAATCGTGGCTGGATCCAGGCTGCCCCGGTCTCTGGT 180
 Db 121 GAGATCAGGGGTOCCAAATCGTGGCTGGATCCAGGCTGCCCCGGTCTCTGGT 180
 Ov 182 GAGATCAGGGGTOCCAAATCGTGGCTGGATCCAGGCTGCCCCGGTCTCTGGT 241
 Db 182 GAGATCAGGGGTOCCAAATCGTGGCTGGATCCAGGCTGCCCCGGTCTCTGGT 241
 Ov 181 GTCCAGGGTGGAAAGCCAGCTCGTCATCTGGGGCTGAGGAACTCTAACACTA 240
 Db 242 GTCCAGGGTGGAAAGCCAGCTCGTCATCTGGGGCTGAGGAACTCTAACACTA 301
 Ov 241 GAGCAGGAACTCATCGTGGCTTATTTGGTGGTCCAGGAATCCAGAGCTTACCTTC 300
 Db 302 GAGCAGGAACTCATCGTGGCTTATTTGGTGGTCCAGGAATCCAGAGCTTACCTTC 361
 Ov 61 CTGCATATAACCGCTCTAGCTGGAGGGCTGATGCCAGGCTGCCCCGGTCTCTGGT 120
 Db 122 CTGCATATAACCGCTCTAGCTGGAGGGCTGATGCCAGGCTGCCCCGGTCTCTGGT 181
 Ov 121 GAGATCAGGGGTOCCAAATCGTGGCTGGATCCAGGCTGCCCCGGTCTCTGGT 180
 Db 182 GAGATCAGGGGTOCCAAATCGTGGCTGGATCCAGGCTGCCCCGGTCTCTGGT 241
 Ov 181 GTCCAGGGTGGAAAGCCAGCTCGTCATCTGGGGCTGAGGAACTCTAACACTA 240
 Db 242 GTCCAGGGTGGAAAGCCAGCTCGTCATCTGGGGCTGAGGAACTCTAACACTA 301
 Ov 241 GAGCAGGAACTCATCGTGGCTTATTTGGTGGTCCAGGAATCCAGAGCTTACCTTC 300
 Db 302 GAGCAGGAACTCATCGTGGCTTATTTGGTGGTCCAGGAATCCAGAGCTTACCTTC 361
 Ov 301 TACCGGGCGGAGCATGGGGCTCACCTCCAGCTTCAGTGGCTGGCTACCTAC 360
 Db 362 TACCGGGCGGAGCATGGGGCTCACCTCCAGCTTCAGTGGCTGGCTACCTAC 421
 Ov 361 CTGTGACACGGCTGCTGAAGCCGATCAGCTGTGAGCTACCCAGCTTCCCGAGATGT 420
 Db 422 CTGTGACACGGCTGCTGAAGCCGATCAGCTGTGAGCTACCCAGCTTCCCGAGATGT 481
 Ov 422 CTGTGACACGGCTGCTGAAGCCGATCAGCTGTGAGCTACCCAGCTTCCCGAGATGT 481
 Ov 421 GGCCTGGATGCCCATACAGACTCTTCACTTCAGGCTGGTGA 468
 Db 482 GGCCTGGATGCCCATACAGACTCTTCACTTCAGGCTGGTGA 529
 RESULT 22
 AR221129 AR221129
 Locus AR221129
 Definition Sequence 6 from patent US 6466191. DNA linear PAT 26-SEP-2002
 Accession AR221129
 Version AR221129.1 GI:23328014
 Keywords
 Source Unknown.
 Organism Unclassified.
 Reference 1 (bases 1 to 2648)

Db 242 GTCCAGGGTggAACCCAGTCTGTCATGGGGGGGAGGAGCTTACACTA 301
 Qy 241 GAGCCAGTGACATGAGGCTCATCTGGTGCAGGAACTCAAGAGCTTC 300
 Db 302 GAGCCAGTGACATGAGGCTCATCTGGTGCAGGAACTCAAGAGCTTC 301
 Qy 301 TACCGCGGGACATGGGCTAACCTCCAGCTTCGAGTCGGCTACCCGGGCTGTC 360
 Db 362 TACCGCGGGACATGGGCTAACCTCCAGCTTCGAGTCGGCTACCCGGGCTGTC 421
 Qy 361 CTGTCGACGCGTGCCTGAAGCCGATCAGCTCTACTCCAGCAGTGACTAG 420
 Db 422 CTGTCGACGCGTGCCTGAAGCCGATCAGCTCTACTCCAGCAGTGACTAG 481
 Qy 421 GGCCTGAATCCCCATCAGGACTCTACTCCAGCAGTGACTAG 468
 Db 482 GGCCTGAATCCCCATCAGGACTCTACTCCAGCAGTGACTAG 529

RESULT 25
 BC024747 BC024747 Homo sapiens interleukin 1 family, member 5 (delta), transcript variant 2, mRNA (cDNA clone MGC:29840 IMAGE:4996939), complete cds. BC024747 BC024747.1 GI:19353229 MGC.
 VERSION KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

Bukay-Yoav, Metzoe, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchoptogires; Primates; Catarrhini; Homidae; Homo;
 1. (bases 1 to 2692)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schaefer, C.P., Bhat, N.K., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heihs, P., Diatchenko, L., Maruska, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toohi-Yuki, S., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilajon, D.K., Muzny, D.M., Sodergren, E.J., Lui, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krywawik, M.J., Skalska, U., Smalius, D.E., Scherch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2692)
 AUTHORS Straubberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.ncbi.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabbs@nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 USA
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu
 Guarante, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louiseged, H., Kowis, C.R., Snead, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: <http://Image.LiML.gov>
 Series: ITRAK Plate: 42 Row: k Column: 16
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 27894309. Location/Qualifiers

FEATURES source

1. -2692
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="txon:9606"
 /clone="MGC:29840 IMAGE:4996939"
 /tissue_type="Placenta, choriocarcinoma"
 /clone_id="NIH MGC_10"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

gene
 1. -2692
 /genes="IL1F5"
 /note="Synonyms: FIL1 (DELTA), FIL1D, IL1RP3, IL1HYL, FIL1, IL1L, MGC29840"
 /db_xref="GeneID:26525"
 /db_xref="MM:60507"
 /gene="IL1F5"
 /codon_start=1
 /product="interleukin 1 family, member 5"
 /protein_id="AAH247.1"
 /db_xref="GI:19353230"
 /db_xref="GeneID:26525"
 /translaton="MVLISGALCFRMKDSALKLYLHNQNLIAAGGLIAGKVKEEISV
 RDMLGTTSPESAAVYPGWPLCTVPEADOPVRLTOLPENGWMAPITDFQCD"
 /ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 2692;
 Best Local Similarity 100.0%; Prod. No. 1; Sae-10; Mismatches 0; Indels 0; Gaps 0;

Db 134 ATGGTCTGAGTGGGGCTGTGCTTCCAAATGAGGACTGGATTGAGGCTTAT 60
 Qy 61 CTGCTATAATACCAAGCTCTAGCTGAGGACTGCTGAGGAAAGGTAA 120
 Db 194 CTGCTATAATACCAAGCTCTAGCTGAGGACTGCTGAGGAAAGGTAA 253
 Qy 121 GAGATCGCTGGTCCCAATCGCTGGCTGATGCCAGCTGCCCCCTCATCTGGT 180
 Db 254 GAGATCAGGGTGGCCCAATCGCTGGCTGAGGCCCTGCTCCCTGCTCATCTGGT 313
 Qy 181 GTCCAGGGTGAAGCCAGTCTGCTCACTGGGAGGAACTCAAGAGCTTACACTA 240
 Db 314 GTCCAGGGTGAAGCCAGTCTGCTCACTGGGAGGAACTCAAGAGCTTACACTA 373
 Qy 241 GAGCCAGTGACATGAGGCTCATCTGGTGCAGGAACTCAAGAGCTTACACTA 300
 Db 374 GAGCCAGTGACATGAGGCTCATCTGGTGCAGGAACTCAAGAGCTTACACTA 433
 Qy 301 TACGGCGGACATGGGCTCACTCCAGCTTCACTGGCTGCTGCTCACTGGGCT 360
 Db 434 TACGGCGGACATGGGCTCACTCCAGCTTCACTGGGCT 493
 Qy 361 CTGTCGACGCTGCTGAAGCCGATCAGCTGTGAGCTACCCAGCTTCCGAGATGT 420
 Db 494 CTGTCGACGCTGCTGAAGCCGATCAGCTGTGAGCTACCCAGCTTCCGAGATGT 553

421 GGCTGAATCCCCATCACAGACTCTACTCCAGCAGTGACTAG 468

Db	554	GGCTGGAATGCCCATCACAGCTTACTCCAGCACTGACTAG	601	Db	463	TACCGCCGGACATGGGCTCACCTCCAGCTGCTGCCAACGGCTGGTC	522
RESULT	56			Qy	351	CCTGAGGGTGCCTGAGGCCATCAGCTGCTGAGCTACCCAGCTCCGAGAATGGT	420
DEFINITION		AF186094	2720 bp mRNA linear homolog (IL1H1)	Db	523	CTGAGCACTGCTGAGGCCATCAGCTGCTGAGCTACCCAGCTCCGAGAATGGT	582
LOCUS		Homo sapiens	interleukin-1 receptor antagonist homolog	Qy	421	GGCTGGAATGCCCATCACAGCTTACTCCAGCTGACTAG	468
ACCESSION		AF186094	mRNA, complete cds.	Db	533	GGCTGGAATGCCCATCACAGCTTACTCCAGCTGACTAG	630
VERSION		AF186094.1	GI:6049804				
KEYWORDS		Homo sapiens (human)					
ORGANISM		Homo sapiens					
SOURCE		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo					
REFERENCE	1	(bases 1 to 2720)					
AUTHORS	Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Drmanac,R. and Ford,J.B.	IL1H1L: A novel interleukin-1 receptor antagonist gene					
TITLE		Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)					
PUBLMED	10512743						
REFERENCE	2	(bases 1 to 2720)					
AUTHORS	Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Drmanac,R. and Ford,J.B.	Submitted (13-SEP-1999) Functional Genomics, HYSEQ Inc., 670 Almanor Ave., Sunnyvale, CA 94086, USA					
JOURNAL							
FEATURES							
source	1..2720	/location/Qualifiers					
gene		/organism="Homo sapiens"					
		/mol_type="mRNA"					
		/db_xref="taxon:9606"					
	1..2720						
		/gene="IL1H1"					
		/note="IL1-1a homolog"					
		/codon_start=1					
		/product="interleukin-1 receptor antagonist homolog"					
		/protein_id="AAF02757.1"					
		/db_xref="GI:6049805"					
		/translation="MVLISGALCFRMKOSALKVLYLHNQNLLAGGLAGKVVKGEERSVVPNRWLDKSLSPVILGQGGSQCLSGVQEQPTLIEPVNIMELYLGAKESKSFTYR					
		RDMLTSSFPESAYPGWFCLTYPBDQPVRLTQLPENGQWNPITDPYFQOCD"					
ORIGIN							
Query	Match	Best Local Similarity 100.0%; Score 468; DB 8; Length 2720; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	ATGCGCTTGTGCGGCGCTGCTCCGATGAGGACTCGCATGAGGCTT	60	COMMENT			
Db	163	ATGGCGCTGATGGCGCTGCTCCGATGAGGCTT	222	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion™ cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence, 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.			
Qy	61	CTGCTATATACCACTCTAGCTGAGGCTGATGCCAGGAAGGTCTAAAGTGA	120	FEATURES			
Db	223	CTGCTATAAACCTAACAGCTCTAGCTGAGGCTGATGCCAGGAAGGTCTAAAGTGA	282	source	1..468	/location/Qualifiers	
Qy	121	GAGATCAGCGGGTCTCCAAATCGGCTGCTGAGATGCCAGCTGCTGCCCTCTCTGGT	180			/organism="synthetic construct"	
Db	283	GAGATCAGCGGGTCTCCAAATCGGCTGCTGAGATGCCAGCTGCTGCCCTCTCTGGT	342			/mol_type="mRNA"	
Qy	181	GTCCAGGGTGAAGCAGCTCTGCTGAGCTTACACTA	240			/db_xref="taxon:32630"	
Db	343	GTCCAGGGTGAAGCAGCTCTGCTGAGCTTACACTA	402			/clone="FL141291.01"	
Qy	241	GAGCCAGTGAATCATGGAGCTCATCTGGTGCAGCTGTCCTCTCTGGT	300			/lab_host="Escherichia coli DH5alpha T1 resistant"	
Db	403	GAGCCAGTGAATCATGGAGCTCATCTGGTGCAGCTTACACTA	462			/note="derived from MGC template"	
Qy	301	TACCGGGGGCATGGCTACCTCCAGCTCTGAGTCGCTGCTACCGGGCTG	360			/codon_start=1	
						/trans_table=1	
						/product="interleukin 1 family member 5"	
						/protein_id="AAK316138.1"	
						/db_xref="UniProtKB:Q310165"	
						/translation="MVLISGALCFRMKOSALKVLYLHNQNLLAGGLAGKVVKGEERSV	
						RDMLTSSFPESAYPGWFCLTYPBDQPVRLTQLPENGQWNPITDPYFQOCD"	
ORIGIN							
Query	Match	Best Local Similarity 99.7%; Score 466.4; DB 11; Length 468; Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					

Db	462	TACGGGGGACATGGGGTCACTCCAGCTGAGTGGCTGCTACCGGGGCTT	521
Qy	360	CTCTGTCAGGGTCCCTGAGGCCATAGCTGCTGAGCTCAGCTCACCAGCTTCCCAGATGG	419
Db	522	CCTGTGACGGTCCCTGAGGCCATAGCTGCTGAGCTCAGCTCACCAGCTTCCCAGATGG	581
Qy	420	TGCTGGATGCCCATCACAGACTTCACTCCAGCTGAGCTGAGCTAG	468
Db	582	TGGCTGGATGCCCATCACAGACTTCACTCCAGCTGAGCTGAGCTAG	630
RESULT 30			
LOCUS	AX675571	AX675571	480 bp
DEFINITION	Sequence 21 from Patent WO2055704.	Sequence 32 from Patent WO012571.	DNA
ACCESSION	AX675571	AX675571.1	GI:29333562
VERSION			PAT 27-MAR-2003
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
AUTHORS	Padigaru, M., Li, L., Zerhouni, B.D., Casman, S.J., Shenoy, S., Verner, C.A., Zhong, M., Gangolli, E.A., Burgess, C.E., Paturyan, M., Verner, C.A., Taylor, S., Tcherniev, V.T., Miller, C.E., Guo, X., Boldog, F.L., Gross, W.M., Alsobrook, J.P., Eidelberg, S., Rothenberg, M.E., Elmer, K., Gerlach, V., Malyankar, J.U., Miletic, I., Pezman, J., Smithson, G., Gunther, E. and Stone, D.J.		
TITLE	Proteins, polynucleotides encoding them and methods of using the same		
JOURNAL	Patent: WO 02055704-A 21 18-JUL-2002; Curagen Corporation (US)		
FEATURES	source		
ORIGIN			
Query Match	75.7%; Score 334.4; DB 6; Length 480;		
Best Local Similarity	85.9%; Pred. No. 9.6e-79;		
Matches	395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;		
Qy	1	ATGGTCTCTGAGTGGGGCTCTTCGAATGAGGACTCGCCATGAGGTTAT	60
Db	1	ATGGTCTCTGAGTGGGGCTCTTCGAATGAGGACTCGCCATGAGGTTAT	60
Qy	61	CTGCATAATACCGACTCTAGTGGGGACTATGCTTCGAATAGGTCTAGTAT	60
Db	61	CTGCATAATACCGACTCTAGTGGGGACTATGCTTCGAATAGGTCTAGTAT	60
Qy	61	CTGCACATAACAGCTCTGCTGGAGGACTCACGAGAGGTATTAAAGGTG	120
Db	61	CTGCACATAACAGCTCTGCTGGAGGACTCACGAGAGGTATTAAAGGTG	120
Qy	121	GAGATCAGCTGGGGCCATCGGGCTGGATCCACCGCTGCCCCGTCACTCTGGT	180
Db	121	GAGATCAGCTGGGGCCATCGGGCTGGATCCACCGCTGCCCCGTCACTCTGGT	180
Qy	181	GTCCAGGGGGAAAGCCAGTGCTCTGCTGCTGAGGAACTCTAACACTA	240
Db	181	GTCCAGGGGGAAAGCCAGTGCTCTGCTGCTGAGGAACTCTAACACTA	240
Qy	241	GAGCCAGTGAACTCATCGAGCTCTATCTGTCAGGAACTCTAACACTA	300
Db	241	GAGCCAGTGAACTCATCGAGCTCTATCTGTCAGGAACTCTAACACTA	300
Qy	301	TACCGGGGGACATGGGGCTACCTCCAGCTTGAGTGGCTGCTGCTGCTGCTG	360
Db	301	TACCGGGGGACATGGGGCTACCTCCAGCTTGAGTGGCTGCTGCTGCTGCTG	360
Qy	361	CTGCGACCTCACCGGAAGCTGAGCTGAGCTCACCTGCTGCTGCTGCTG	420
Db	361	CTGCGACCTCACCGGAAGCTGAGCTGAGCTCACCTGCTGCTGCTGCTG	420
Qy	421	GCCTGGAAATGCCCATCACAGACTCTACTCCAGCTGAGCTGAGCTAG	468
Db	421	GCCTGGAAATGCCCATCACAGACTCTACTCCAGCTGAGCTGAGCTAG	468
RESULT 31			
LOCUS	AX69335	AX69335	468 bp
DEFINITION	Sequence 32 from Patent WO012571.	DNA	
ACCESSION	AX69335	AX69335.1	GI:12519200
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Sciuromorchi; Muroidea; Muridae; Murinae; Mus.		
AUTHORS	Ford, J. and Pace, A.		
TITLE	A interleukin-1 receptor antagonist and uses thereof		
JOURNAL	Patent: WO 0105571-A 32 11-JAN-2001; HYSEQ, INC. (US)		
FEATURES	Location/Qualifiers		
ORIGIN			
Query Match	75.0%; Score 351.2; DB 6; Length 468;		
Best Local Similarity	84.4%; Pred. No. 6.2e-78;		
Matches	395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;		
Qy	1	ATGGTCTCTGAGTGGGGCTCTTCGAATGAGGACTCCCATGAGGCTTAT	60
Db	1	ATGGTCTCTGAGTGGGGCTCTTCGAATGAGGACTCCCATGAGGCTTAT	60
Qy	61	CTGCATAATACCGACTCTAGTGGGGACTATGCTTCGAATAGGTCTAGTAT	60
Db	61	CTGCATAATACCGACTCTAGTGGGGACTATGCTTCGAATAGGTCTAGTAT	60
Qy	61	CTGCACATAACAGCTCTGCTGGAGGACTCACGAGAGGTATTAAAGGTG	120
Db	61	CTGCACATAACAGCTCTGCTGGAGGACTCACGAGAGGTATTAAAGGTG	120
Qy	121	GAGATCAGCTGGGGCCATCGGGCTGGATCCACCGCTGCCCCGTCACTCTGGT	180
Db	121	GAGATCAGCTGGGGCCATCGGGCTGGATCCACCGCTGCCCCGTCACTCTGGT	180
Qy	181	GTCCAGGGGGAAAGCCAGTGCTCTGCTGCTGAGGAACTCTAACACTA	240
Db	181	GTCCAGGGGGAAAGCCAGTGCTCTGCTGCTGAGGAACTCTAACACTA	240
Qy	241	GAGCCAGTGAACTCATCGAGCTCTATCTGTCAGGAACTCTAACACTA	300
Db	241	GAGCCAGTGAACTCATCGAGCTCTATCTGTCAGGAACTCTAACACTA	300
Qy	301	TACCGGGGGACATGGGGCTACCTCCAGCTTGAGTGGCTGCTGCTGCTG	360
Db	301	TACCGGGGGACATGGGGCTACCTCCAGCTTGAGTGGCTGCTGCTGCTG	360
Qy	361	CTGCGACCTCACCGGAAGCTGAGCTGAGCTCACCTGCTGCTGCTG	420
Db	361	CTGCGACCTCACCGGAAGCTGAGCTGAGCTCACCTGCTGCTGCTG	420
Qy	421	GCCTGGAAATGCCCATCACAGACTCTACTCCAGCTGAGCTGAGCTAG	468
Db	421	GCCTGGAAATGCCCATCACAGACTCTACTCCAGCTGAGCTGAGCTAG	468
RESULT 32			
LOCUS	AF230378	AF230378	471 bp
DEFINITION	Mus musculus interleukin-1 delta mRNA, complete cds.	mRNA	linear
ACCESSION	AF230378	AF230378	ROD 01-NOV-2001
Qy	295	ACCTCTTACGGGGGACATGGGGCTACCTCCAGCTGAGTGGCTGCTGCTG	354
Db	301	ACCTCTTACGGGGGACATGGGGCTACCTCCAGCTGAGTGGCTGCTGCTG	360
Qy	355	TGGTCTCTGCAAGGGCTGAGGCCATGAGCTTCCAGCTCCAGCTCCAG	414
Db	355	TGGTCTCTGCAAGGGCTGAGGCCATGAGCTTCCAGCTCCAGCTCCAG	414

VERSION AP230378.1 GI:9651790

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 471)

AUTHORS Debets, R., Timans, J.C., Heme, B., Zurawski, S., Sana, T.R., Io, S., Wagner, J., Edwards, G., Clifford, R., Menon, S., Bazan, J.F. and Kastlein, R.A.

TITLE Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2

JOURNAL J. Immunol. 167 (3), 1440-1446 (2001)

PUBMED 1146633

REFERENCE 2 (bases 1 to 471)

AUTHORS Kastlein, R.A., Timans, J.C., Sana, T., Debets, R. and Bazan, F.

TITLE Direct Submission

JOURNAL Submitted (01-FEB-2000) Molecular Biology, DNAX Research Institute, 901 California Ave, Palo Alto, CA 94304, USA

FEATURES Location/Qualifiers

source

1. 471

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

1. 471

/note="IL-1delta; cytokine"

/codon_start=1

/product="interleukin-1 delta"

/protein_id="AAFI275_1"

/db_xref="GI:9651791"

/translation="MIVLUSGALCPRMKDSALKVLYLHNQLLAGLHAEKVKGEBIS VVPRNADASLSPVILQVGGSQCLSGCTEKOPILKEPVNIMELVIGAKESKSFTFV RDMGLTSSFESAYPQGMFLCSPEADQPVRUQIPEDPDAPITDYFQOCD"

ORIGIN

Query Match 75.0%; Score 351.2; DB 9; Length 471;

Best Local Similarity 84.4%; Pred. No. 6.2e-78;

Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 60

Db 4 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 63

Db 61 CTGCTAAATACCGCTCTAGCTGGAGGCTGCATCGAGGAGGTCTTAAAGTGA 120

Db 64 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 123

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGATGCGTGTGCCCCCTCATCTGGT 180

Db 124 GAGATCAGCTGTGTCCTAACATCGGGCACTGGATGCGTGTGCCCCCTCATCTGGC 183

Qy 181 GTCCAGGGTGAAGCCAGTGCCTCATCTGGAGGATCAAGGCTCACCTC 240

Db 184 GTTCAGAGGAGGAGCAGCTCTAACCTGGAGGATCAAGGCTCACCTC 243

Qy 241 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 300

Db 244 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 303

Qy 301 TACCGGGCGGACATGGGCTCACCTCAGCTTCAGTGGCTGCGCTGCTACCGGCTGCTGTC 360

Db 304 TACCGGGCGGATATGGCTTACTTCAGCTTCGATCTGGCTTACCCAGGCTGGTC 363

Qy 361 CTGGCAGCTGCCGATGCTGAGCTGAGCTCACCTGGAGGATCTGGAGGACCC 420

Db 364 CTCTGCACTTACCGGAGCTGAGCTACTAGATCCCTGGAGGACCC 423

Qy 421 GGCTGGAAATGCCCATCGAGCTCTACTCCAGCTGCTGAGCTGCTGAGCTGAGCTGAGTAG 468

Db 424 GGCTGGAGGCTCCATCGAGCTCTACTCCAGCTGCTGAGCTGAGTAG 471

RESULT 33

REFERENCE AP200495

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

source

1 (bases 1 to 1283)

/note="IL-1delta; cytokine"

/codon_start=1

/product="interleukin-1 family"

/protein_id="AAE69251_1"

/db_xref="GI:769118"

/translation="MVLSGALCPRMKDSALKVLYLHNQLLAGLHAEKVKGEBIS VVPRNADASLSPVILQVGGSQCLSGCTEKOPILKEPVNIMELVIGAKESKSFTFV RDMGLTSSFESAYPQGMFLCSPEADQPVRUQIPEDPDAPITDYFQOCD"

ORIGIN

Query Match 75.0%; Score 351.2; DB 9; Length 1283;

Best Local Similarity 84.4%; Pred. No. 6e-78;

Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 60

Db 110 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 169

Qy 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Db 61 CTGCTAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 289

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGTGGTGGATCCAGCTGCGCTGCTGCTGTC 180

Db 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGTGGTGGATCCAGCTGCGCTGCTGCTGTC 180

Db 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Qy 181 GTCCAGGGTGAAGCCAGTGCCTCATCTGGAGGATCAAGGCTCACCTC 240

Db 184 GTTCAGAGGAGGAGCAGCTCTAACCTGGAGGATCAAGGCTCACCTC 243

Qy 241 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 300

Db 244 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 303

Qy 301 TACCGGGCGGACATGGGCTCACCTCAGCTTCAGTGGCTGCGCTGCTACCGGCTGCTGTC 360

Db 304 TACCGGGCGGATATGGCTTACTTCAGCTTCGATCTGGCTTACCCAGGCTGGTC 363

Qy 361 CTGGCAGCTGCCGATGCTGAGCTGAGCTACTAGATCCCTGGAGGACCC 420

Db 364 CTCTGCACTTACCGGAGCTGAGCTACTAGATCCCTGGAGGACCC 423

Qy 421 GGCTGGAAATGCCCATCGAGCTCTACTCCAGCTGCTGAGCTGCTGAGTAG 468

Db 424 GGCTGGAGGCTCCATCGAGCTCTACTCCAGCTGCTGAGTAG 471

RESULT 33

REFERENCE AP200495

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

source

1 (bases 1 to 1283)

/note="IL-1delta; cytokine"

/codon_start=1

/product="interleukin-1 family"

/protein_id="AAE69251_1"

/db_xref="GI:769117"

/translation="MVLSGALCPRMKDSALKVLYLHNQLLAGLHAEKVKGEBIS VVPRNADASLSPVILQVGGSQCLSGCTEKOPILKEPVNIMELVIGAKESKSFTFV RDMGLTSSFESAYPQGMFLCSPEADQPVRUQIPEDPDAPITDYFQOCD"

ORIGIN

Query Match 75.0%; Score 351.2; DB 9; Length 1283;

Best Local Similarity 84.4%; Pred. No. 6e-78;

Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 60

Db 110 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 169

Qy 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Db 61 CTGCTAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 289

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGTGGTGGATCCAGCTGCGCTGCTGCTGTC 180

Db 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGTGGTGGATCCAGCTGCGCTGCTGCTGTC 180

Db 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Qy 181 GTCCAGGGTGAAGCCAGTGCCTCATCTGGAGGATCAAGGCTCACCTC 240

Db 184 GTTCAGAGGAGGAGCAGCTCTAACCTGGAGGATCAAGGCTCACCTC 243

Qy 241 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 300

Db 244 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 303

Qy 301 TACCGGGCGGACATGGGCTCACCTCAGCTTCAGTGGCTGCGCTGCTACCGGCTGCTGTC 360

Db 304 TACCGGGCGGATATGGCTTACTTCAGCTTCGATCTGGCTTACCCAGGCTGGTC 363

Qy 361 CTGGCAGCTGCCGATGCTGAGCTGAGCTACTAGATCCCTGGAGGACCC 420

Db 364 CTCTGCACTTACCGGAGCTGAGCTACTAGATCCCTGGAGGACCC 423

Qy 421 GGCTGGAAATGCCCATCGAGCTCTACTCCAGCTGCTGAGCTGCTGAGTAG 468

Db 424 GGCTGGAGGCTCCATCGAGCTCTACTCCAGCTGCTGAGTAG 471

RESULT 33

REFERENCE AP200495

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

source

1 (bases 1 to 1283)

/note="IL-1delta; cytokine"

/codon_start=1

/product="interleukin-1 family"

/protein_id="AAE69251_1"

/db_xref="GI:769117"

/translation="MVLSGALCPRMKDSALKVLYLHNQLLAGLHAEKVKGEBIS VVPRNADASLSPVILQVGGSQCLSGCTEKOPILKEPVNIMELVIGAKESKSFTFV RDMGLTSSFESAYPQGMFLCSPEADQPVRUQIPEDPDAPITDYFQOCD"

ORIGIN

Query Match 75.0%; Score 351.2; DB 9; Length 1283;

Best Local Similarity 84.4%; Pred. No. 6e-78;

Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 60

Db 110 ATGGTCTCTGAGTGGGCACTATGCTTCGAGGATTCGCGATTGAGGTTAT 169

Qy 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Db 61 CTGCTAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 289

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGTGGTGGATCCAGCTGCGCTGCTGCTGTC 180

Db 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Qy 121 GAGATCAGCGCTGGTCCCAATCGGGCACTGGTGGTGGATCCAGCTGCGCTGCTGCTGTC 180

Db 170 CTGCAAAATACCGCTCTAGCTGGAGGAGGTCTTAAAGTGA 229

Qy 181 GTCCAGGGTGAAGCCAGTGCCTCATCTGGAGGATCAAGGCTCACCTC 240

Db 184 GTTCAGAGGAGGAGCAGCTCTAACCTGGAGGATCAAGGCTCACCTC 243

Qy 241 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 300

Db 244 GAGCCAGTGAACATCTGGAGCTATCTGGTCCAGGATCAAGGCTCACCTC 303

Qy 301 TACCGGGCGGACATGGGCTCACCTCAGCTTCAGTGGCTGCGCTGCTACCGGCTGCTGTC 360

Db 304 TACCGGGCGGATATGGCTTACTTCAGCTTCGATCTGGCTTACCCAGGCTGGTC 363

Qy 361 CTGGCAGCTGCCGATGCTGAGCTGAGCTACTAGATCCCTGGAGGACCC 420

Db 364 CTCTGCACTTACCGGAGCTGAGCTACTAGATCCCTGGAGGACCC 423

Qy 421 GGCTGGAAATGCCCATCGAGCTCTACTCCAGCTGCTGAGCTGCTGAGTAG 468

Db 424 GGCTGGAGGCTCCATCGAGCTCTACTCCAGCTGCTGAGTAG 471

RESULT 38	424	GGCTGGGATGCTCCCATCACAGACTTCTACTTCAGCAGTGTGAC	470
AX080399	AX080399	Sequence 11 from Patent WO0105974.	465 bp DNA linear PAT 22-FEB-2001
LOCUS	AX080399		
DEFINITION	Sequence 11 from Patent WO0105974.		
ACCESSION	AX080399		
VERSION	AX080399.1	GI:13159845	
KEYWORDS			
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	Sciurrognathi; Murioidea; Muridae; Murinae; Mus.		
AUTHORS	1 Nicklin, M. and Barton, J.		
TITLE	The IL-11 gene and polypeptide products		
JOURNAL	Patent: WO 0105974-A 11-25-JAN-2001; Interleukin Genetics, Inc. (US)		
FEATURES	Source		
ORIGIN			
Query Match	74.4%; Score 348.2; DB 6; Length 465;		
Best Local Similarity	84.3%; Pred. No. 3.5e-77;		
Matches	392; Conservative		
	0; Mismatches		
	73; Indels		
	0; Gaps		
Qy	1 ATGGCTCTAGTGGGGCGCTGCTCCGAAATGAGGACTGGATTAGGGCTTAT	60	
Db	1 ATGGCTCTAGTGGGGCGACTATGCTCCGAAATGAGGATTAGGGCTTAT	60	
Qy	61 CTGCATTAATACCGCTCTAGCTGGAGGGCTGATGAGGGAGTCAATTAGTGAA	120	
Db	61 CTGCACAAATACCGACTGCTGGCTGAGAGAGTGAA	120	
Qy	121 GAGCTAGGGTGGAGACCGAGCTGCTCATGGGCTGGCCAGGGCTACCTGGT	180	
Db	121 GAGATCAGTGTGCCAATCAGCTGGAGTGGCTGCACTGCTGCACTGGC	180	
Qy	181 GTCCAGGGTGGCCATCGGGCTGCTGAGAGGAGCTAACACTA	240	
Db	181 GTTCAAGAGGAACCGAGCTGCTTGGGAGAAGGGCCATTCTGAACCT	240	
Qy	241 GAGCCAGTGAATCTATGGCTTACCTGGGAGGAAATCAAGAGCTTCACCTC	300	
Db	241 GAGCCAGTGAATCTATGGCTTACCTGGGAGGAAATCAAGAGCTTCACCTC	300	
Qy	301 TACGGGGGACATGGGGTCACTCCAGCTCGTCACTGGCTGCTACCCGGAGTGGTC	360	
Db	301 TACCGGGGATATGGGCTTACCTCCAGCTTCACTGGCTGCTACCCGGCTGTC	360	
Qy	361 CTGTCACCTCAGGGAGCTGACCTGGCTGAGTGGT	420	
Db	361 CTGTCACCTCAGGGAGCTGACCTGGCTGAGTGGT	420	
Qy	421 GGCTGGAAATGCCCATCACAGACTTCTACTTCAGCAGTGTGAC	465	
Db	421 GGCTGGAAATGCCCATCACAGACTTCTACTTCAGCAGTGTGAC	465	
RESULT 39	BD124060	BD124060	468 bp DNA linear PAT 18-SEP-2002
LOCUS	BD124060		
DEFINITION	DNA and polypeptide of IL-1-delta.		
ACCESSION	BD124060		
VERSION	BD124060.1	GI:23219005	
KEYWORDS	JP 200250046-A/1.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
RESULT 40	BD211432	BD211432	338 bp DNA linear PAT 17-JUL-2003
LOCUS	BD211432		
DEFINITION	A novel interleukin-1 receptor antagonist and uses thereof.		
ACCESSION	BD211432		
VERSION	BD211432.1	GI:33021202	
KEYWORDS	JP 2002510492A/1.		
SOURCE	Homo sapiens (human)		

ORGANISM	Homo sapiens	JOURNAL	Patent: US 6337072-A 1 08-JAN-2002;
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FEATURES	Location/Qualifiers
REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrini;	Source	1..357
1 (bases 1 to 338)	Hominidae; Homo.		/organism="unknown"
AUTHORS	Ford,J. and Pace,A.		/mol_type="unassigned DNA"
JOURNAL	A novel interleukin-1 receptor antagonist and uses thereof	ORIGIN	
COMMENT	HYSE, INC		
OS	Homo sapiens (human)		
PN	JP 2002510492-A/1		
PD	JP 2002510492-A/1		
PR	05-APR-1999 JP 2000542457		
03-APR-1998 US 09/055010, 15-MAY-1998 US 09/079909 PR	Query Match	51.9%;	Score 243;
20-MAY-1998 US 09/082364, 19-JUN-1998 US 09/09818 PR	Best Local Similarity	100.0%;	Pred. No. 1..4e-50;
31-JUL-1998 US 09/121688, 13-JAN-1999 US 09/229591 PR	Mismatches	0;	Indels 0;
17-FEB-1999 US 09/251370	Gaps 0;		
PI	JOHN FORD, ANN PACE	QY	
PC	C12N15/09, A61K39/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,	226 CCGACTCTAACCTAGACGCCAGTGAACTCATGGGCTCACCTCCACCTGAGTCGCTGCC 285	
PC	C12N15/19, C12N5/10, C12Q1/68, G01N33/50, G01N33/566, G01N33/68, PC	1 CCGACTCTAACCTAGACGCCAGTGAACTCATGGGCTCACCTCCACCTGAGTCGCTGCC 60	
C12N15/00	CC A novel interleukin-1 receptor antagonist and uses thereof	286 AAGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 345	
FT	FT	1 C12N15/02, C12N5/00	
Key	A novel interleukin-1 receptor antagonist and uses thereof	61 AAGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 120	
Source	Location/Qualifiers	1. .338	
FEATURES	/organism='Homo sapiens (human)'		
source	1. .338		
ORIGIN	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/ab_xref="taxon:9606"		
Query Match	51.9%;	Score 243;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 1..4e-50;	Length 338;
Matches	243;	Indels 0;	Mismatches 0;
	Conservative	Gaps 0;	
QY	226 CCGACTCTAACCTAGACGCCAGTGAACTCATGGGCTCACCTCCACCTGAGTCGCTGCC 285	Db	
Db	1 CCGACTCTAACCTAGACGCCAGTGAACTCATGGGCTCACCTCCACCTGAGTCGCTGCC 60	QY	
QY	286 AAGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 345	Db	
Db	61 AAGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 120	QY	
QY	346 TACCGGGCTGGTCTCTGGCTGACCGTGTGAAGCCGATCAGCTGTCAGCTACCCAG 405	Db	
Db	121 TACCGGGCTGGTCTCTGGCTGACCGTGTGAAGCCGATCAGCTGTCAGCTACCCAG 180	QY	
QY	406 CTTCCCGAGAATGTTGGCTGGATGCCCCATACAGCTTACTTCAGCAGTGTGAC 465	Db	
Db	181 CTTCCCGAGAATGTTGGCTGGATGCCCCATACAGCTTACTTCAGCAGTGTGAC 240	QY	
QY	466 TAG 468	Db	
Db	241 TAG 243	QY	
Db	241 TAG 243	Db	
RESULT 42			
AR221126			
LOCUS	AR221126		
DEFINITION	Sequence 1 from patent US 6426191.		
ACCESSION	AR221126		
VERSION	AR221126.1 GI:23328011		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 357)		
AUTHORS	Ford,J. and Pace,A.		
TITLE	Assays involving an IL-1 receptor antagonist		
JOURNAL	Patent: US 6426191-A 1 30-JUL-2002;		
	HySeq, Inc.; Sunnyvale, CA		
FEATURES	Location/Qualifiers		
source	1. .357		
ORIGIN	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	51.9%;	Score 243;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 1..4e-50;	Length 357;
Matches	243;	Indels 0;	Mismatches 0;
	Conservative	Gaps 0;	
QY	226 CCGACTCTAACCTAGACGCCAGTGAACTCATGGGCTCACCTCCACCTGAGTCGCTGCC 285	Db	
Db	1 CCGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 60	QY	
QY	286 AAGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 345	Db	
Db	61 AAGACTCTAACCTCTACGGGGACATGGGCTCACCTCCACCTGAGTCGCTGCC 120	QY	
QY	346 TACCGGGCTGGTCTCTGGCTGACCGTGTGAAGCCGATCAGCTGTCAGCTACCCAG 405	Db	
Db	121 TACCGGGCTGGTCTCTGGCTGACCGTGTGAAGCCGATCAGCTGTCAGCTACCCAG 180	QY	
QY	406 CTTCCCGAGAATGTTGGCTGGATGCCCCATACAGCTTACTTCAGCAGTGTGAC 465	Db	
Db	181 CTTCCCGAGAATGTTGGCTGGATGCCCCATACAGCTTACTTCAGCAGTGTGAC 240	Db	
RESULT 41			
AR181992			
DEFINITION	Sequence 1 from patent US 6337072.		
ACCESSION	AR181992		
VERSION	AR181992.1 GI:20224908		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 357)		
AUTHORS	Ford,J. and Pace,A.		
TITLE	Interleukin-1 receptor antagonist and recombinant production thereof		

QV 466 TAG 468
 Db 241 TAG 243

ORIGIN
 misc_feature 1. . 357
 /note="n = A,T,C or G"

RESULT 43
 AR302954 AR302954 sequence 1 from patent 357 bp DNA linear PAT 12-JUN-2003
 DEFINITION 1.0%; Pred. No. 1.4e-50; Length 357;
 LOCUS 0; Indels 0; Gaps 0;
 ACCESSION 0; Mismatches 0;
 VERSION 0;
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1. (bases 1 to 357)
 AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.
 TITLE Interleukin-1 receptor antagonist and uses thereof
 JOURNAL Patent: US 6541623-A 1 01-APR-2003;
 Hyseq, Inc., Sunnyvale, CA
 FEATURES Location/Qualifiers
 source 1. . 357
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 51.9%; Score 243; DB 6; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 243; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 226 CCGACTCTAACACTAGAGCCGTGAGCATCTGGAGCTTCTGGCCAGGAATCC 285
 Db 1 CCGACTCTAACACTAGAGCCGTGAGCATCTGGAGCTTCTGGCCAGGAATCC 60

QV 286 AAGAGCTTCACTCTACCGGGGAGATGGGTCACCTCAGCTGGCTCC 345
 Db 61 AAGAGCTTCACTCTACCGGGGAGATGGGTCACCTCAGCTGGCTCC 120

QY 346 TACCCGGCTGGTCTCTGACGGGCTCTGAGCCGATCTGAGCTGGCTCC 405
 Db 121 TACCCGGCTGGTCTCTGACGGGCTCTGAGCCGATCTGAGCTGGCTCC 180

QV 406 CTTCGGAGAATGGCTGAGCTTCTACTTCAGCAGTGAC 465
 Db 181 CTTCGGAGAATGGCTGAGCTTCTACTTCAGCAGTGAC 240

QY 466 TAG 468
 Db 241 TAG 243

ORIGIN
 misc_feature 1. . 357
 /note="n = A,T,C or G"

RESULT 45
 BD211433 BD211433 985 bp DNA linear PAT 17-JUL-2003
 DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
 LOCUS BD211433
 ACCESSION BD211433.1 GI:33021203
 VERSION JP 2002510492-A/2.
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1. (bases 1 to 985)
 AUTHORS Ford, J. and Pace, A.
 TITLE A novel interleukin-1 receptor antagonist and uses thereof
 JOURNAL HYSEQ, INC.
 FEATURES OS Homo sapiens (human)
 PN JP 2002510492-A/2
 PD 09-APR-2002
 PR 05-APR-1999 JP 2000542457
 PR 03-APR-1998 US 09/082364-19-JUN-1998 US 09/099818 PR
 20-MAY-1998 US 09/127699, 13-JAN-1999 US 09/229591 PR
 31-JUL-1998 US 09/125370
 PT JOHN FORD, ANN PACE
 PC C12N15/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,
 PC C12N1/19,
 PC C12N1/21, C12N5/10, C12Q1/68, G01N33/50, G01N33/566, G01N33/68, PC
 C12N15/00,
 PC A61K37/02, C12N5/00
 CC A novel interleukin-1 receptor antagonist and uses thereof PR
 FEATURES source
 FT Key source
 FT Location/Qualifiers
 FT /organism="Homo sapiens (human)".
 ORIGIN
 Query Match 51.9%; Score 243; DB 6; Length 985;
 Best Local Similarity 100.0%; Pred. No. 1.3e-50;

REFERENCE 1. . 357
 AUTHORS Ford, J. and Pace, A.
 TITLE A interleukin-1 receptor antagonist and uses thereof
 JOURNAL Patent: WO 0102571-A 1 11-JAN-2001;
 HYSEQ, INC. (US)
 FEATURES Location/Qualifiers
 source 1. . 357
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /ab_xref="taxon:9606",
 /db_xref="unassigned DNA"

Matches 243; conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 CCGACTCTAACACTAGAGCCAGTGCACATCATGGAGCTCTATCTGGCCAGGAATCC 285
 Db 1 CCGACTCTAACACTAGAGCCAGTGCACATCATGGAGCTCTATCTGGCCAGGAATCC 60

Qy 286 AAGAGCTTCACTTCTACCGGGGACATGGGCTCACCTCAGCTTCAAGTCAGTCAGCTGCC 345
 Db 61 AAGAGCTTCACTTCTACCGGGGACATGGGCTCACCTCAGCTTCAAGTCAGTCAGTCAGCTGCC 120

Qy 346 TACCCGGGTGTTCTCTGTGCGACGGCATGGCTGCGAGCTTCAAGTCAGTCAGTCAGCTGCC 405
 Db 121 TACCCGGGTGTTCTCTGTGCGACGGCATGGCTGCGAGCTTCAAGTCAGTCAGTCAGCTGCC 180

Qy 406 CTTCCGAGAGATGGTGGCTGGAATGGCCCATCACAGACTTCTACTTCAGCAGTGAC 465
 Db 181 CTTCCGAGAGATGGTGGCTGGAATGGCCCATCACAGACTTCTACTTCAGCAGTGAC 240

Qy 466 TAG 468
 Db 241 TAG 243

RESULT 46

AR181993
 LOCUS AR181993 985 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 2 from patent US 63337072.
 ACCESSION AR181993
 VERSION AR181993.1 GI:20224909
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 985)
 AUTHORS Ford, J. and Pace, A.
 TITLE Interleukin-1 receptor antagonist and recombinant production
 JOURNAL patent: US 63337072-A 2 08-JAN-2002;
 FEATURES source
 ORIGIN
 Query Match 51.9%; Score 243; DB 6; Length 985;
 Best Local Similarity 100.0%; Pred. No. 1.3e-50; Mismatches 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 CCGACTCTAACACTAGAGCCAGTGCACATCATGGGCTCACCTCAGCTTCAAGTCAGTCAGCTGCC 285
 Db 61 AAGAGCTTCACTTCTACCGGGGACATGGGCTCACCTCAGCTTCAAGTCAGTCAGTCAGCTGCC 120

Qy 346 TACCCGGGTGTTCTCTGTGCGACGGCATGGCTGCGAGCTTCAAGTCAGTCAGTCAGCTGCC 405
 Db 121 TACCCGGGTGTTCTCTGTGCGACGGCATGGCTGCGAGCTTCAAGTCAGTCAGTCAGCTGCC 180

Qy 406 CTTCCGAGAGATGGTGGCTGGAATGGCCCATCACAGACTTCTACTTCAGCAGTGAC 465
 Db 181 CTTCCGAGAGATGGTGGCTGGAATGGCCCATCACAGACTTCTACTTCAGCAGTGAC 240

Qy 466 TAG 468
 Db 241 TAG 243

RESULT 48

AR302955
 LOCUS AR302955 985 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 2 from patent US 6541623.
 ACCESSION AR302955
 VERSION AR302955.1 GI:3169555
 KEYWORDS
 SOURCE Unknown.
 Unclassified.
 1 (bases 1 to 985)
 AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.
 TITLE Interleukin-1 receptor antagonist and uses thereof
 JOURNAL Patent: US 6541623-A 2 01-APR-2003;
 Hyseq, Inc.; Sunnyvale, CA
 FEATURES source
 ORIGIN
 Query Match 51.9%; Score 243; DB 6; Length 985;
 Best Local Similarity 100.0%; Pred. No. 1.3e-50; Mismatches 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 CCGACTCTAACACTAGAGCCAGTGCACATCATGGGCTCACCTCAGCTTCAAGTCAGTCAGCTGCC 285
 Db 61 CCGACTCTAACACTAGAGCCAGTGCACATCATGGGCTCACCTCAGCTTCAAGTCAGTCAGTCAGCTGCC 120

Qy 346 TACCCGGGTGTTCTCTGTGCGACGGCATGGCTGCGAGCTTCAAGTCAGTCAGTCAGCTGCC 405
 Db 121 TACCCGGGTGTTCTCTGTGCGACGGCATGGCTGCGAGCTTCAAGTCAGTCAGTCAGCTGCC 180

Qy 406 CTTCCGAGAGATGGTGGCTGGAATGGCCCATCACAGACTTCTACTTCAGCAGTGAC 465
 Db 181 CTTCCGAGAGATGGTGGCTGGAATGGCCCATCACAGACTTCTACTTCAGCAGTGAC 240

Qy 466 TAG 468
 Db 241 TAG 243

RESULT 47

AR221127 AR221127 985 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 2 from patent US 6426191.

RESULT 49

AX069305 AX069305 Sequence 2 from Patent WO0102571. 985 bp DNA linear PAT 25-JAN-2001

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

1. Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE AUTHORS TITLE JOURNAL

1. (bases 1 to 295) Goddard,A. and Pan,J. GENETECH INC OS Homo sapiens (human)

COMMENT

PN JP 2002533122-A 8 08-OCT-2002; GENETECH INC

PD 22-DEC-1999 JP 2000591188

PR 23-DEC-1998 US 60/113430,22-JAN-1999 US 60/116843 PR

13-APR-1999 US 60/123122 PI AUDREY GODDARD, JAMES SAN PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12P21/02, C12P21/08, C12N15/00, C12N15/00 CC unknown base Key FH Location/Qualifiers FT unsure

FEATURES SOURCE

1. .295 Location/Qualifiers

/organism="Homo sapiens" /mol_type="genomic DNA" /ab_xref="taxon:9606"

CDS

<1..243

/note="unnamed protein product"

/codon_start=1

/protein_id="CAC27297.1"

/db_xref="GI:12279178"

/translation="PTITLEPVINIMELYGAKESKSFPTFYRDRMGLTSSPESAAVPGWFLCTVPEADQPVRLTQLPENGWNAPITDFYFQCD"

ORIGIN

Query Match Best Local Similarity 99.6%; Pred. No. 8 2e-49; Length 295; Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTCTCTAGATGGGGCCCTCTGGCTCGGAATGAGGATCTCGCCATGAGGCTTAT 60

DB 59 ATGGTCTCTAGATGGGGCCCTCTGGCTCGGAATGAGGATCTCGCCATGAGGCTTAT 117

QY 61 CTGATATAAACAGCTCTAGCTGGAGGGCTCATGGAGGAGGTATAAAGGAA 120

DB 118 CTGCATATAAACAGCTCTAGCTGGAGGGCTCATGGAGGAGGTATAAAGGAA 177

QY 121 GAGATCAGCTGGTCCCAATCGTGGTGGTGGATGCCACCCCTGTCATCTGGT 180

DB 178 GAGATCAGCTGGTCCCAATCGTGGTGGTGGATGCCACCCCTGTCATCTGGT 237

QY 181 GTCCAGGTGGAGCCAGTGGCTCTAGTGGGTGGAGCAGCCACTCTAAC 237

DB 238 GTCCAGGTGGAGCCAGTGGCTCTAGTGGGTGGAGCAGCCACTCTAAC 294

Query Match Best Local Similarity 100.0%; Pred. No. 1 3e-50; Matches 243; conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CGACTCTAACCTAGAGSCAGTGACATCATGGAGCTCTATCTCTGGGCCAAGAAC 285

DB 1 CGCACTTAACTAGAGCCGAGCATCATGGAGCTCTATCTGGGCCAAGAAC 60

QY 285 AGAGCTTCACTCTAACCGGCGAGCATGGGCTCACCTCAGCTCTGGAGGGCTGCC 345

DB 61 AGAGCTTCACTCTAACCGGCGAGCATGGGCTCACCTCAGCTCTGGAGGGCTGCC 120

QY 346 TACCGGGCTGTCTCTGACCGGTGCTGAGCCGATCAGCTCTGGCTAGACCTACCCAG 405

DB 121 TACCGGGCTGTCTCTGACCGGTGCTGAGCCGATCAGCTCTGGCTAGACCTACCCAG 180

QY 406 CTTCGGAGAAATGGGGCTGCGAATGCCCCATCAACAGCTTCTACTTCAGCAGTGTGAC 465

DB 181 CTTCGGAGAAATGGGGCTGCGAATGCCCCATCAACAGCTTCTACTTCAGCAGTGTGAC 240

QY 466 TAG 468

DB 241 TAG 243

RESULT 50

BB263574

Locus BD263574 Definition IL-1 related polypeptides. 295 bp DNA linear PAT 17-JUL-2003

Accession BD263574

Version BD263574.1 GI:33073342

Keywords JP 2002533122-A/8

Source Homo sapiens (human)

Organism Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

Reference 1. (bases 1 to 295)

Authors Goddard,A. and Pan,J.

Title GENETECH INC

Journal OS Homo sapiens (human)

Comment PN JP 2002533122-A 8 08-OCT-2002; GENETECH INC

Patent: JP 2002533122-A 8 08-OCT-2002;

PD 22-DEC-1999 JP 2000591188

PR 23-DEC-1998 US 60/113430,22-JAN-1999 US 60/116843 PR

13-APR-1999 US 60/123122 PI AUDREY GODDARD, JAMES SAN PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12P21/02, C12P21/08, C12N15/00, C12N15/00 CC unknown base Key FH Location/Qualifiers FT unsure

Features Source

1. .295 Location/Qualifiers

/organism="Homo sapiens" /mol_type="genomic DNA" /ab_xref="taxon:9606"

Origin

Query Match Best Local Similarity 99.6%; Pred. No. 8 2e-49; Length 295; Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTCTCTAGATGGGGCCCTCTGGCTCGGAATGAGGATCTCGCCATGAGGCTTAT 60

DB 59 ATGGTCTCTAGATGGGGCCCTCTGGCTCGGAATGAGGATCTCGCCATGAGGCTTAT 117

QY 61 CTGATATAAACAGCTCTAGCTGGAGGGCTCATGGAGGAGGTATAAAGGAA 120

DB 118 CTGCATATAAACAGCTCTAGCTGGAGGGCTCATGGAGGAGGTATAAAGGAA 177

QY 121 GAGATCAGCTGGTCCCAATCGTGGTGGTGGATGCCACCCCTGTCATCTGGT 180

DB 178 GAGATCAGCTGGTCCCAATCGTGGTGGTGGATGCCACCCCTGTCATCTGGT 237

QY 181 GTCCAGGTGGAGCCAGTGGCTCTAGTGGGTGGAGCAGCCACTCTAAC 237

DB 238 GTCCAGGTGGAGCCAGTGGCTCTAGTGGGTGGAGCAGCCACTCTAAC 294

Search completed: January 27, 2006, 21:00:29

Job time : 3030 secs

GenCore version 5.1.6
copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using bw model
Run on: January 27, 2006, 19:03:18 ; Search time 3070 Seconds
(without alignments)
7132.363 Million cell updates/sec

Title: US-09-612-921B-3
Perfect score: 468
Sequence: 1 atggctcttgagt-ggggct.....acttccagcagtggtgacttag 468

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 300 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_ntc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_g881:
10: gb_g882:
11: gb_g883:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	468	10	AY413262 Homo Sapi DR004557 TC115434
2	468	100.0	762	8	DR004557
3	468	100.0	858	2	BI090567
4	468	100.0	2605	4	CR613851
5	467.6	99.9	985	1	AL545100
6	467	99.8	632	7	CVO29389
7	463.2	99.0	468	10	AY413263
8	458.9	97.9	2726	2	BI089828
9	351.2	75.0	1051	4	AK009741
10	351.2	75.0	1199	4	AK009877
11	349.6	74.7	862	6	CB590160
12	343.2	73.3	885	6	CB598411
13	340.8	72.8	2841	4	AK014576
14	338.4	72.3	708	5	BY709379
15	338	72.2	414	7	CR742272
16	333.2	71.2	1531	4	AK010020
17	327	69.9	439	10	AY413264
18	271	57.9	338	5	BX477558
19	259.8	55.5	898	6	CB194288
20	248.2	53.0	691	5	BY754693
21	238.8	51.0	686	5	BY708859
22	208.6	44.6	382	8	W08205

23	166.6	35.6	348	5	BY109350
24	161.6	34.5	343	5	BY107750
25	160	34.2	689	7	CK947864
26	160	34.2	702	7	CK952430
27	153	32.7	689	6	CD368042
28	131	28.0	784	9	CC526753
29	125.2	26.8	501	6	CR116914
30	123.6	26.4	621	5	BY714015
31	111.8	23.9	593	6	CD694328
32	110.6	23.6	884	5	BX416842
33	110.2	23.5	470	10	AY402945
34	110.2	23.5	615	7	CR994235
35	110.2	23.5	864	3	BI49907
36	110.2	23.5	1581	4	CR616993
37	110.2	23.5	1644	4	CR616671
38	110.2	23.5	1666	4	CR65915
39	109	23.3	735	6	CD468328
40	108.6	23.3	572	7	CY027812
41	108.6	23.2	757	5	BX424058
42	108.6	23.2	932	5	BX406556
43	108.6	23.2	938	2	BEE63703
44	108.6	23.2	955	3	BM00948
45	108.2	23.1	900	4	AL540334
46	108.2	23.1	1069	1	AL554778
47	107	22.9	403	3	BM818991
48	107	22.9	640	2	BG288796
49	103.8	22.2	120	2	BG987216
50	103.8	22.2	435	11	DQ43278
51	103.8	22.2	900	4	AY026753
52	102.2	21.8	976	3	BM921822
53	101.6	21.5	435	11	DQ043279
54	100.2	21.4	611	6	CD466328
55	100.2	21.4	610	6	CD471267
56	100.2	21.4	664	6	CD462656
57	100.2	21.4	675	6	CD468330
58	100.2	21.4	737	6	CD468474
59	99.8	21.3	726	3	BT765516
60	99.2	21.2	519	4	AY610557
61	99.2	21.2	686	8	DN381477
62	99.2	21.2	832	3	BI512352
63	99	21.2	671	5	BW959334
64	99	21.2	686	7	CJ007558
65	98.6	21.1	526	6	CD471100
66	98.6	21.1	550	6	CD471862
67	98.6	21.1	551	6	CD465665
68	98.6	21.1	552	6	CD471284
69	98.6	21.1	554	6	CD472222
70	98.6	21.1	564	6	CD469052
71	98.6	21.1	574	6	CD468320
72	98.6	21.1	578	6	CD470841
73	98.6	21.1	580	6	CD471738
74	98.6	21.1	581	6	CD465060
75	98.6	21.1	586	6	CD465215
76	98.6	21.1	590	6	CD465334
77	98.6	21.1	591	6	CD465268
78	98.6	21.1	598	6	CD471729
79	98.6	21.1	601	6	CD469756
80	98.6	21.1	602	6	CD465590
81	98.6	21.1	608	6	CD465227
82	98.6	21.1	608	6	CD469122
83	98.6	21.1	611	6	CD465811
84	98.6	21.1	611	6	CD472338
85	98.6	21.1	613	6	CD471113
86	98.6	21.1	615	6	CD465365
87	98.6	21.1	616	6	CD471699
88	98.6	21.1	624	6	CD463325
89	98.6	21.1	626	6	CD469064
90	98.6	21.1	627	6	CD470864
91	98.6	21.1	627	6	CD469704
92	98.6	21.1	627	6	CD469727
93	98.6	21.1	628	6	CD472233
94	98.6	21.1	629	6	CD465892
95	98.6	21.1	630	6	CD469095

CD469095	Leukos2_1
CD469095	Leukos2_2
CD469095	Leukos2_3
CD469095	Leukos2_4
CD469095	Leukos2_5
CD469095	Leukos2_6
CD469095	Leukos2_7
CD469095	Leukos2_8
CD469095	Leukos2_9
CD469095	Leukos2_10
CD469095	Leukos2_11
CD469095	Leukos2_12
CD469095	Leukos2_13
CD469095	Leukos2_14
CD469095	Leukos2_15
CD469095	Leukos2_16
CD469095	Leukos2_17
CD469095	Leukos2_18
CD469095	Leukos2_19
CD469095	Leukos2_20
CD469095	Leukos2_21
CD469095	Leukos2_22
CD469095	Leukos2_23
CD469095	Leukos2_24
CD469095	Leukos2_25
CD469095	Leukos2_26
CD469095	Leukos2_27
CD469095	Leukos2_28
CD469095	Leukos2_29
CD469095	Leukos2_30
CD469095	Leukos2_31
CD469095	Leukos2_32
CD469095	Leukos2_33
CD469095	Leukos2_34
CD469095	Leukos2_35
CD469095	Leukos2_36
CD469095	Leukos2_37
CD469095	Leukos2_38
CD469095	Leukos2_39
CD469095	Leukos2_40
CD469095	Leukos2_41
CD469095	Leukos2_42
CD469095	Leukos2_43
CD469095	Leukos2_44
CD469095	Leukos2_45
CD469095	Leukos2_46
CD469095	Leukos2_47
CD469095	Leukos2_48
CD469095	Leukos2_49
CD469095	Leukos2_50
CD469095	Leukos2_51
CD469095	Leukos2_52
CD469095	Leukos2_53
CD469095	Leukos2_54
CD469095	Leukos2_55
CD469095	Leukos2_56
CD469095	Leukos2_57
CD469095	Leukos2_58
CD469095	Leukos2_59
CD469095	Leukos2_60
CD469095	Leukos2_61
CD469095	Leukos2_62
CD469095	Leukos2_63
CD469095	Leukos2_64
CD469095	Leukos2_65
CD469095	Leukos2_66
CD469095	Leukos2_67
CD469095	Leukos2_68
CD469095	Leukos2_69
CD469095	Leukos2_70
CD469095	Leukos2_71
CD469095	Leukos2_72
CD469095	Leukos2_73
CD469095	Leukos2_74
CD469095	Leukos2_75
CD469095	Leukos2_76
CD469095	Leukos2_77
CD469095	Leukos2_78
CD469095	Leukos2_79
CD469095	Leukos2_80
CD469095	Leukos2_81
CD469095	Leukos2_82
CD469095	Leukos2_83
CD469095	Leukos2_84
CD469095	Leukos2_85
CD469095	Leukos2_86
CD469095	Leukos2_87
CD469095	Leukos2_88
CD469095	Leukos2_89
CD469095	Leukos2_90
CD469095	Leukos2_91
CD469095	Leukos2_92
CD469095	Leukos2_93
CD469095	Leukos2_94
CD469095	Leukos2_95
CD469095	Leukos2_96
CD469095	Leukos2_97
CD469095	Leukos2_98
CD469095	Leukos2_99
CD469095	Leukos2_100

96	98.6	21.1	631	6	CD465198	Leukon1_2	169	96	20.5	422	5	BX257557
97	98.6	21.1	631	6	CD471123	LeukoS5_4	170	96	20.5	493	6	CD455440
98	98.6	21.1	632	6	CD465349	Leukon1_3	171	96	20.5	524	6	CD465440
99	98.6	21.1	632	6	CD471706	LeukoS6_4	172	96	20.5	577	5	BW951605
100	98.6	21.1	635	6	CD465263	Leukon1_2	173	96	20.5	787	5	BW957508
101	98.6	21.1	635	6	CD470944	LeukoS5_3	174	95.8	20.5	397	2	BE46054
102	98.6	21.1	635	6	CD468174	LeukoS3_1	175	95.6	20.4	635	1	AW262191
103	98.6	21.1	637	6	CD468174	LeukoS2_1	176	95.6	20.4	747	8	DR423704
104	98.6	21.1	638	6	CD465095	Leukon1_2	177	95.6	20.4	1073	1	AL549965
105	98.6	21.1	638	6	CD465213	Leukon1_1	178	95.6	20.4	1653	4	CR425646
106	98.6	21.1	640	6	CD465088	Leukon1_1	179	95.4	20.4	548	6	CD465466
107	98.6	21.1	640	6	CD468221	LeukoS3_1	180	95.4	20.4	552	6	CD455688
108	98.6	21.1	641	6	CD464253	Leukon4_2	181	95.4	20.4	612	6	CD45571
109	98.6	21.1	648	6	CD469528	LeukoS2_2	182	95.4	20.4	552	6	CD472212
110	98.6	21.1	649	6	CD470580	LeukoS3_1	183	95.4	20.4	570	6	CD45471
111	98.6	21.1	649	6	CD470580	LeukoS4_6	184	95.4	20.4	575	6	CD472063
112	98.6	21.1	650	6	CD469384	Leukon1_1	185	95.4	20.4	519	3	B1961215
113	98.6	21.1	651	6	CD465603	Leukon1_5	186	95.4	20.4	611	6	CD470551
114	98.6	21.1	656	6	CD468855	LeukoS3_7	187	95.4	20.4	612	6	CD472073
115	98.6	21.1	664	6	CD469378	LeukoS2_8	188	95.4	20.4	624	6	CD470145
116	98.6	21.1	668	6	CD468109	LeukoS3_3	189	95.4	20.4	626	6	CD465027
117	98.6	21.1	669	6	CD471103	LeukoS5_4	190	95.4	20.4	625	6	CD465898
118	98.6	21.1	671	6	CD469212	LeukoS2_2	191	95.4	20.4	632	6	CD465780
119	98.6	21.1	678	6	CD471002	Leukon1_2	192	95.4	20.4	636	6	CD45368
120	98.6	21.1	679	6	CD468554	LeukoS3_7	193	95.4	20.4	644	6	CD465445
121	98.6	21.1	681	6	CD468234	LeukoS3_1	194	95.4	20.4	645	6	CD470695
122	98.6	21.1	681	6	CD469261	LeukoS2_2	195	95.4	20.4	651	6	CD465026
123	98.6	21.1	681	6	CD469556	LeukoS2_4	196	95.4	20.4	654	6	CD465899
124	98.6	21.1	684	6	CD467302	LeukoS1_3	197	95.4	20.4	664	6	CD465350
125	98.6	21.1	687	6	CD468361	LeukoS3_2	198	95.4	20.4	664	6	CD465547
126	98.6	21.1	708	6	CD466354	LeukoS2_5	199	95.4	20.4	664	6	CD465907
127	98.6	21.1	716	6	CD469371	LeukoS2_3	200	95.4	20.4	669	6	CD465595
128	98.6	21.1	751	6	CD465024	Leukon1_8	201	95.4	20.4	669	6	CD465575
129	98.6	21.1	752	6	CD469744	LeukoS2_8	202	95.4	20.4	755	6	CD465555
130	98.6	21.1	768	6	CD469568	LeukoS2_4	203	95.4	20.4	768	6	CD465034
131	98.6	21.1	772	6	CD469830	LeukoS2_5	204	95.2	20.3	349	6	CD465356
132	98.6	21.1	778	6	CD466354	Leukon2_3	205	95.2	20.3	531	6	CD465931
133	98.6	21.1	809	6	CD469371	LeukoS2_3	206	95	20.3	432	7	CK615408
134	98.6	21.1	809	6	CD469848	Leukon1_8	207	94.8	20.3	470	10	AY42946
135	97.6	20.9	510	6	CD470139	LeukoS4_1	208	94.6	20.2	435	8	W78043
136	97.6	20.9	512	6	CD470313	LeukoS4_3	209	94.4	20.2	472	6	CD465371
137	97.6	20.9	531	1	AW951593	EST33363	210	94.2	20.1	589	6	CD465072
138	97.6	20.9	598	8	DN333540	LTR35349	211	94	20.1	507	6	CD465564
139	97.6	20.9	607	6	CD469566	LeukoS2_4	212	94	20.1	525	7	CK838069
140	97.6	20.9	638	1	AJ746765	AJ746765	213	94	20.1	549	2	BE780905
141	97.6	20.9	650	6	CD469744	Leukon1_3	214	93.8	20.0	550	6	CD472024
142	97.6	20.9	695	3	BP45359	BP45359	215	93.8	20.0	554	6	CD465479
143	97.6	20.9	700	3	BP453893	BP453893	216	93.8	20.0	554	6	CD472017
144	97.6	20.9	784	7	BP436742	BP436742	217	93.8	20.0	558	6	CD465346
145	97.6	20.9	508	6	CD470837	LeukoS5_2	218	93.8	20.0	574	6	CD470105
146	97.6	20.7	510	6	CD469536	LeukoS2_4	219	93.8	20.0	657	6	CD465185
147	97.6	20.7	550	6	CD471712	LeukoS6_4	220	93.8	20.0	658	6	CD465777
148	97.6	20.7	561	6	CD46928	LeukoS2_2	221	93.5	20.0	658	1	AW446284
149	97.6	20.7	571	6	CD472084	LeukoS6_3	222	93.6	20.0	536	8	DN440706
150	97.6	20.7	611	6	CD469429	LeukoS2_3	223	93.6	20.0	572	8	DN440858
151	97.6	20.7	622	6	CD464241	Leukon4_2	224	93.6	20.0	574	8	CD471928
152	97.6	20.7	632	6	CD470567	LeukoS4_5	225	93.6	20.0	694	6	CD465191
153	97.6	20.7	633	6	CD470997	LeukoS5_3	226	93.6	20.0	696	6	CD465582
154	97.6	20.7	716	6	CD465601	Leukon1_5	227	93.5	20.0	777	6	CA307607
155	97.6	20.7	732	6	CD465589	Leukon1_5	228	93.4	20.0	487	6	CD471578
156	96.8	20.7	454	6	CD470526	LeukoS4_5	229	93.2	20.0	572	8	DN440858
157	96.8	20.7	473	6	CD465685	Leukon1_6	230	93.2	20.0	574	8	CD471928
158	96.8	20.7	529	6	CD469521	LeukoS2_4	231	93.2	19.9	638	6	CD465913
159	96.8	20.7	546	6	CD466498	Leukon2_4	232	93	19.9	824	3	BI762103
160	96.8	20.7	586	6	CD469246	LeukoS2_2	233	92.4	19.7	371	2	BI020838
161	96.8	20.7	592	6	CD470536	Leukon1_5	234	92.4	19.7	470	10	AY402947
162	96.8	20.7	607	6	CD465454	Leukon1_4	235	92.2	19.7	507	6	CD472242
163	96.8	20.7	612	6	CD471874	LeukoS6_2	236	92.2	19.7	592	8	CX73034
164	96.8	20.7	656	6	CD469281	Leukon2_2	237	92.2	19.7	607	6	CD465883
165	96.8	20.7	679	6	CD4649395	LeukoS2_3	238	92.2	19.7	653	5	BY748178
166	96.8	20.7	690	6	CD469712	LeukoS2_8	239	92.2	19.7	653	5	BY750171
167	96.8	20.7	711	6	CD469229	Leukon2_2	240	92.2	19.7	678	5	BY748887
168	96.6	20.6	532	6	CD472204	LeukoS6_1	241	92.2	19.7	678	5	BY764111

DEFINITION	TC115434 Human placenta, large insert, pCMV expression library Homo sapiens cDNA clone TC115434 5', similar to Homo sapiens interleukin 1 family, member 5 (delta) (IL1F5), transcript variant 1, mRNA sequence.
ACCESSION	DR004557
VERSION	DR004557.1 GI:6626430
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
TITLE	High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
JOURNAL	Unpublished (2005)
COMMENT	Contact: Kovacs, KF High throughput cDNA cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: cdna@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access.
FEATURES	Location/Qualifiers
source	1. .762 'organism="Homo sapiens'" 'mol_type="mRNA'" 'db_xref="taxon:9606'" 'clone="TC115434"' 'tissue_type="Placenta"' 'clone_lib="Human placenta, large insert, pCMV expression library"' 'note="vector: pCMV6-XL4; Site_1: EcoRI; Site_2: xba1; Sall compatible end ligation; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"'
ORIGIN	Query Match 100 %; Score 468; DB 8; Length 762; Best Local Similarity 100.0%; Pred. No. 1.7e-118; Mismatches 468; Conservative 0; Indels 0; Gaps 0;
Qy	1 ATGGTCTCTGAGTGGGGCTGCTTCGAATGAAGGACTCGCATGAGGTCTTAT 60
Db	69 ATGGTCTCTGAGTGGGGCTGCTTCGAATGAAGGACTCGCATGAGGTCTTAT 128
Qy	61 CTGCAATAAACCAAGCTCTAGCTGGAGGGCTGATCGAGGAAGGTATTAAGGTGAA 120
Db	129 CTGCAATAAACCAAGCTCTAGCTGGAGGGCTGATCGAGGAAGGTATTAAGGTGAA 188
Qy	121 GAGATCAGCTGCTCCAACTGGTCTGAGCTGGAGGGCTGCTTCGAATGAAGGACTCGCATGAGGTCTTAT 180
Db	189 GAGATCAGCTGCTCCAACTGGTCTGAGCTGGAGGGCTGATCGAGGAAGGTATTAAGGTGAA 248
Qy	181 GTCAGGGTGAAGCCAGTGCCTGTCATGGGGCTGATCGAGGAAGGTATTAAGGTGAA 240
Db	249 GTCCAGGGTGAAGCCAGTGCCTGATGTCAGGGCTGATCGAGGAAGGTATTAAGGTGAA 308
REFERENCE	241 GAGCCAGTGAACATCATGGAGCTCTATCTGGTCAAGGAATCAAAGAGCTTACCTTC 300
AUTHORS	309 GAGCCAGTGAACATCATGGAGCTCTATCTGGTCAAGGAATCAAAGAGCTTACCTTC 368
COMMENT	3.01 TACCGGGGACATGGGCTCACCTCCAGTCAGTCGCTGCCTACCCGGCTGGTC 360
FEATURES	3.69 TACCGGGGACATGGGCTCACCTCCAGTCAGTCGCTGCCTACCCGGCTGGTC 428
source	3.61 CTGTCACAGTGGCTGAGCGATCAGCTGTCAGACTACCCAGCTCCGAGATGT 420
Qy	429 CTGTCACAGTGGCTGAGCGATCAGCTGTCAGACTACCCAGCTCCGAGATGT 488
Db	421 GGCTGGATACTCCCATACAGACATCTACTCCAGCAGTGTACTAG 468
Qy	489 GGCCTGAACTGCCCATACAGACTCTACTCCAGCAGTGTACTAG 536
RESULT	3
source	B1090567
COMMENT	B1090567
FEATURES	LOCUS 60285574 1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996939 5'
source	DEFINITION mRNA sequence.
COMMENT	B1090567
FEATURES	ACCESSION B1090567.1 GI:14508897
source	VERSION EST.
COMMENT	EST.
FEATURES	ORGANISM Homo sapiens (human)
source	Homo sapiens
COMMENT	Homo sapiens
FEATURES	Mammalia; Eutheria; Burchontogires; Primates; Catarrhini; Hominoidea; Homo.
source	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Burchontogires; Primates; Catarrhini;
COMMENT	Unpublished (1999)
FEATURES	CONTACT: Robert Strauberg, Ph.D.
source	Email: cgs@ra-mail.nih.gov
COMMENT	Tissue Procurement: ATCC
FEATURES	COMMENT: CDNA library Preparation: Life Technologies, Inc.
source	CDNA library Arrayed by: Incyte Genomics, Inc.
COMMENT	DNA Sequencing by: Incyte Genomics, Inc.
FEATURES	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: http://image.lnl.gov/clone_xref="taxon:9606"
source	Plate: LIAW11023 row: c column: 20
COMMENT	High quality sequence stop: 670.
FEATURES	Location/Qualifiers
source	1. .858
COMMENT	/organism="Homo sapiens"
FEATURES	/mol_type="mRNA"
source	/db_xref="taxon:9606"
COMMENT	/clone=IMAGE:4996939"
FEATURES	/cell_line="MCC36"
source	/lab_host="DH10B"
COMMENT	/clone lib="NIH MGC 10"
FEATURES	/note="Organ: cervix" vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
source	Average insert size 1.5 kb. Library prepared by Life Technologies."
ORIGIN	Query Match 100 %; Score 468; DB 2; Length 858; Best Local Similarity 100.0%; Pred. No. 1.7e-118; Mismatches 468; Conservative 0; Indels 0; Gaps 0;
Qy	1 ATGGTCTCTGAGTGGGGCTGCTTCGAATGAAGGACTCGCATGAGGTCTTAT 60
Db	135 ATGGTCTCTGAGTGGGGCTGCTTCGAATGAAGGACTCGCATGAGGTCTTAT 194
Qy	61 CTGCAATAAACCAAGCTCTAGCTGGAGGGCTGATCGAGGAAGGTATTAAGGTGAA 120
Db	195 CTGCAATAAACCAAGCTCTAGCTGGAGGGCTGATCGAGGAAGGTATTAAGGTGAA 254

QY	121	GAGATCGCGGGTCCCCAATGGTACTGGATGCCAGCTGTCCTGGTACCTCTGGT	180	QY	61	CTGCATATAACCGCTCTAGCTGGGGCTGCATGCCAGGAGCTATTAAGGTGAA	120
Db	255	GAGATCGCGGGTCCCCAATGGTACTGGATGCCAGCTGTCCTGGTACCTCTGGT	314	Db	163	CTGCATATAACCGCTCTAGCTGGGGCTGCATGCCAGGAGCTATTAAGGTGAA	222
QY	181	GTCGAGGTGAAAGCCAGTCGCTGTCAGTGGGGCTGGGGAGCCGACTCTAACATA	240	QY	121	GAGATCGCGGGTCCCCAATGGTACTGGATGCCAGGAGCTATTAAGGTGAA	180
Db	315	GTCCAGGGTGAAGGCCAGTCGCTGTCAGTGGGGCTGGGGAGCCGACTCTAACATA	374	Db	223	GAGATCGCGGGTCCCCAATGGTACTGGATGCCAGGAGCTATTAAGGTGAA	282
QY	241	GAGCCAGGTGAACTATGGAGCTCTTCTGGCTGCAAGGATCCAGAGCTTCACCTC	300	QY	181	GTCGAGGTGAAAGCCAGTCGCTGTCAGTGGGGCTGGGGAGCCGACTCTAACATA	240
Db	375	GAGCCAGGTGAACTATGGAGCTTCAGCTGAGCTCTGCTGCAAGGATCCAGAGCTTCACCTC	434	Db	283	GTCCAGGGTGAAGGCCAGTCGCTGTCAGTGGGGCTGGGGAGCCGACTCTAACATA	342
QY	301	TACCGCCGGGACATGGGGCTTACCTCAGCTCGAGTCAGCTGAGCTTACCCGGCTGTC	360	QY	241	GAGCCAGGTGAAAGCCAGTCGCTGTCAGTGGGGCTGGGGAGCCGACTCTAACATA	300
Db	435	TACCGCCGGGACATGGGGCTTACCTCAGCTGAGCTGAGCTGAGCTGAGCTGGCT	494	Db	343	GAGCCAGGTGAACTATGGAGCTTCAGCTGAGCTGAGCTGAGCTGAGCTAACCTC	402
QY	361	CTGTGCAAGGGCTGAGGCTAGCTGAGCTTACCCGGCTGTC	420	QY	301	TACCGCCGGGACATGGGGCTTACCTCAGCTGAGCTGAGCTGAGCTGAGCTAACCTC	360
Db	495	CTGTGCAAGGGCTGAGGCTAGCTGAGCTGAGCTGAGCTGAGCTGAGCTAACCTC	554	Db	403	TACCGCCGGGACATGGGGCTTACCTCAGCTGAGCTGAGCTGAGCTGAGCTAACCTC	462
QY	421	GCCTGCAATGCCCTATCACAGACTCTACTTCCAGCAGTGACTAG	468	QY	361	CTGTGCAAGGGCTGAGGCTAGCTGAGCTGAGCTGAGCTGAGCTAACCTC	420
Db	555	GCCTGCAATGCCCTATCACAGACTCTACTTCCAGCAGTGACTAG	602	Db	463	CTGTGCAAGGGCTGAGGCTAGCTGAGCTGAGCTGAGCTAACCTC	522
RESULT 4							
CR613851	CR613851	2605 bp mRNA linear HTC 21-JUL-2004	DEFINITION	CR613851	2605 bp mRNA linear HTC 21-JUL-2004	DEFINITION	CR613851
LOCUS	CR613851	Full-length cDNA clone CS0D1013YA07 of Placenta Cot 25-normalized	VERSION	CR613851.1	GT:50494658	VERSION	CR613851.1
KEYWORDS	HCRC; CNSLT cDNA.		KEYWORDS			KEYWORDS	
SOURCE	Homo sapiens (human)		ORGANISM	Homo sapiens		ORGANISM	Homo sapiens
REFERENCE			REFERENCE			REFERENCE	
AUTHORS	Li, W.B., Gruber,C., Jessee,J. and Polayes,D.		AUTHORS			AUTHORS	
TITLE	Full-length cDNA libraries and normalization		TITLE			TITLE	
JOURNAL	Unpublished		JOURNAL			JOURNAL	
REMARK			COMMENT			COMMENT	
REFERENCE			REFERENCE			REFERENCE	
AUTHORS			AUTHORS			AUTHORS	
TITLE			TITLE			TITLE	
JOURNAL			JOURNAL			JOURNAL	
FEATURES			COMMENT			COMMENT	
source			COMMENT			COMMENT	
ORIGIN			COMMENT			COMMENT	
Query Match	100.0%	Score 468; DB 4; Length 2605;					
Best Local Similarity	100.0%	DB 4; Length 2605;					
Matches	468	Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT	60				
Db	103	ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT	162				
ORIGIN							
FEATURES							
source							
ORIGIN							

Query Match 100.0%; Score 468; DB 4; Length 2605; Best Local Similarity 100.0%; DB 4; Length 2605; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT 60

Db 103 ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT 162

ORIGIN

Query Match 100.0%; Score 468; DB 4; Length 2605; Best Local Similarity 100.0%; DB 4; Length 2605; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT 60

Db 103 ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT 162

ORIGIN

Query Match 100.0%; Score 468; DB 4; Length 2605; Best Local Similarity 100.0%; DB 4; Length 2605; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT 60

Db 103 ATGGCTCTGAGGGGGCTGTGCTCCGAGTGAAGGAGCTGGCATGAGGTCTTAT 162

Query Match	Score	DB	Length	Best Local Similarity	No. of Mismatches	Indels	Gaps	Comments	
QY 1	99.9%	DB 1	985	99.8%	0	0	0	Matched; Conservative	
Db 103	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
QY 61	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 163	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
QY 121	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 223	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
QY 181	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 283	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
QY 241	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 343	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 301	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 403	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
QY 361	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 463	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
QY 421	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
Db 523	99.9%	Db 1	985	99.8%	0	0	0	Matched; Conservative	
RESULT 6									
CV029389	CV029389	CV029389	CV029389	CV029389	CV029389	CV029389	CV029389	CV029389	
LOCUS	8151	Full Length cDNA from the Mammalian Gene Collection	8152	8153	8154	8155	8156	8157	
DEFINITION	CV029389								
ACCESSION	CV029389								
VERSION	1	2	3	4	5	6	7	8	
KEYWORDS	EST.								
SOURCE	Homo sapiens (human)								
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo
COMMENT	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	Human ORFome, Version 1.1: a Platform for Reverse Proteomics	
Marc Vidal	Laboratory	Marc Vidal							
Dana Farber Cancer Institute	1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA	Dana Farber Cancer Institute							
Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	
REFERENCE	1	(bases 1 to 632)	2	3	4	5	6	7	
AUTHORS	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.	Ruai, J.F., Hirao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosembach, P., Vidalain, P.O., Clingerman, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bokas, S., Doucette-Stamm, L., Le Peuch, C., Vandenhoute, J., Chisick, M.E., Albaum, S., Hill, D.E. and Vidal, M.
COMMENT	Genome Res. (2004) In press								
Marc Vidal	Laboratory	Marc Vidal							
Dana Farber Cancer Institute	1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA	Dana Farber Cancer Institute							
Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	Fax: 617 632 5739	Tel: 617 632 5180	
REFERENCE	1	(bases 1 to 468)	2	3	4	5	6	7	
AUTHORS	Marc Vidal								
COMMENT	Tag (OST) of Gateway Entry construct. Each cloned ORF	results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers	PCR Primers	FORWARD: ATGGCTCTGAGTGGGGC	BACKWARD: TAGTCACTGCTGAGTGGAGTGA	Insert Length: 632	Std Error: 45.00		

AUTHORS	SOURCE	Homo sapiens (human)
REFERENCE	ORGANISM	Homo sapiens
Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J., Adams,M.D. and Cargill,M.	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Cetarrhini; Hominoidea; Homo.	
Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios	1 (bases 1 to 726), NIH-MGC http://mgc.nci.nih.gov/	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
PUBLISHED	14671302	
2 (bases 1 to 468)	Unpublished (1999)	
REFERENCE	Comment: Robert S. Strausberg, Ph.D.	
2	Email: cgsrbs@mail.nih.gov	
Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J., Adams,M.D. and Cargill,M.	CDNA Library Preparation: Life Technologies, Inc.	
Direct Submission	CDNA Library Arrayed by: Incyte Genomics, Inc.	
JOURNAL	DNA Sequencing by: Incyte Genomics, Inc.	
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov	
FEATURES	Plate: IJAM1021 row: n column: 17	
gene	High quality sequence stop: 709.	
gene	/organism="Homo sapiens"	
gene	/mol_type="genomic DNA"	
gene	/db_xref="taxon:9598"	
gene	/locus_tag="HCM4832"	
ORIGIN		
Query Match		
Best Local Similarity	99.0%	Score 463.2; DB 10; Length 468;
Matches	465;	Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 ATGGTCTGAGGAGGGCGCTGCTTCGATGAAAGACTCGCATGAAAGTGCTTAT	60
Db	1 ATGGTCTGAGGAGGGCGCTGCTTCGATGAAAGACTCGCATGAAAGTGCTTAT	60
Qy	61 CTGCAATTAAACCAAGCTCTACTGGAGGTGATCGAGCGGCTATCCCGTGTATCCGGT	120
Db	61 CTGCAATTAAACCAAGCTCTACTGGAGGTGATCGAGCGGCTATCCCGTGTATCCGGT	120
Qy	121 GAGATCAGCGCTGCCAAAGGTCGATGAAAGACTCGCATGAAAGTGCTTAT	180
Db	121 GAGATCAGCGCTGCCAAAGGTCGATGAAAGACTCGCATGAAAGTGCTTAT	180
Qy	181 GTCAGGGTGAAGGCCAGTGCCTGATGTCGGTGGCGGAGCGACTAACTA	240
Db	181 GTCAGGGTGAAGGCCAGTGCCTGATGTCGGTGGCGGAGCGACTAACTA	240
Qy	241 GAGCCAGTGAACATCATGAGACTCTATCTGTCGCAAGGATCCAGACTTC	300
Db	241 GAGCCAGTGAACATCATGAGACTCTATCTGTCGCAAGGATCCAGACTTC	300
Qy	301 TACCGGGGACATGGGGCTAACCTCGAGCTCGAGTGGTGCCTACCCGGCTGTC	360
Db	301 TACCGGGGACATGGGGCTAACCTCGAGCTCGAGTGGTGCCTACCCGGCTGTC	360
Qy	361 CTGTGCAAGGGCTCTGAGGCCATCAGCTTCCAGAATGTT	420
Db	361 CTGTGCAAGGGCTCTGAGGCCATCAGCTTCCAGAATGTT	420
Qy	421 GCTGCTGATGCCCTCAAGACTCTACTCCAGCAGTGACTAG	468
Db	421 GCTGCTGATGCCCTCAAGACTCTACTCCAGCAGTGACTAG	468
RESULT 8		
B109828	B109828	726 bp mRNA linear EST 20-JUN-2001
LOCUS	6085501F1	mRNA sequence
DEFINITION	6085501F1 NTH_MGC_10 Homo sapiens cDNA clone IMAGE:4996432	
ACCESSION	B109828	
VERSION	B109828.1	GT:14508158
KEYWORDS	EST.	
RESULT 9		
Qy	431 CCCCATCACAGACTCTACTCCAGCTGACTAG	468
Db	421 CCCCATCACAGACTCTACTCCAGCTGACTAG	458
Qy	371 TCCCTGAGCGATCAGCTCTAGCTCAGCTGAGCTGCTGAGATG	430
Db	361 TCCCTGAGCGATCAGCTCTAGCTCAGCTGAGCTGCTGAGATG	420
Qy	251 ACATCATGGAGCTTACTTGTGCAAGGATCCAGGTTCACTTC	310
Db	241 ACATCATGGAGCTTACTTGTGCAAGGATCCAGGTTCACTTC	300
Qy	311 ACATGGGGCTACCTCCAGCTGAGCTGCTGAGCTGCTGAGCT	370
Db	301 ACATGGGGCTACCTCCAGCTGAGCTGCTGAGCTGCTGAGCT	360
Qy	371 TCCCTGAGCGATCAGCTCTAGCTCAGCTGAGCTGCTGAGATG	430
Db	361 TCCCTGAGCGATCAGCTCTAGCTCAGCTGAGCTGCTGAGATG	420

VERSION	AK009741	LOCUS	AK009741
KEYWORD	HTC; CAP trapper	DEFINITION	1051 bp mRNA linear HTC 03-APR-2004
SOURCE	Mus musculus (house mouse)	MISCELLANEOUS	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310041K07 product:interleukin 1 family, member 5 (delta), full insert sequence.
ACCESSION	AK009741	ACCESSION	AK009741.1 GI:12044719
JOURNAL	10349636	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
REFERENCE	1	REFERENCE	Carninci, P. and Hayashizaki, Y.
AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	PUBLMED	11042159
REFERENCE	2	REFERENCE	Yoneida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kishida, A. and Hayashizaki, Y.
AUTHORS	RIKEN integrated sequence analysis (RSA) system-384-format sequencing pipeline with 384 multicapillary sequencer	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	PUBLMED	11042159
REFERENCE	3	REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitamura, T., Tadhiro, H., Itoh, M., Sumi, N., Ishii, M., Nakamura, S., Hazama, M., Nishime, T., Harada, A., Yamamoto, R., Matsumoto, S., Sakaguchi, S., Inegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachiki, M., Yoneida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kishida, A. and Hayashizaki, Y.
AUTHORS	Genome Res. 10 (11), 1757-1771 (2000)	TITLE	Group Phase I & II Team.
JOURNAL	Group Phase I & II Team.	PUBLMED	11076861
REFERENCE	4	REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
AUTHORS	Functional annotation of a full-length mouse cDNA collection	TITLE	Nature 409, 685-690 (2001)
JOURNAL	Nature 409, 685-690 (2001)	PUBLMED	11076861
REFERENCE	5	REFERENCE	The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	TITLE	Nature 420, 563-573 (2002)
JOURNAL	Nature 420, 563-573 (2002)	PUBLMED	11076861
REFERENCE	6	REFERENCE	(bases 1 to 1051)
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Eukawa, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Imoto, I., Ishii, Y., Itoh, M., Izawa, M., Kasutawa, T., Kato, H., Kojima, Y., Konno, Y., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, K., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibusawa, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Togawa, A., Takahashi, F., Tanaka, T., Tominaga, Y., Toya, T., Yamamura, T., Yasuishi, A., Yoshida, K., Yoshimura, M., Muramatsu, M. and Hayashizaki, Y.	TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan; E-mail: genome-res@riken.jp, URL: http://genome.gen.riken.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216	PUBLMED	11076861
COMMENT	Please visit our web site (http://genome.gsc.riken.jp/) for further details.		
	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken		

Best Match	Similarity	Score	Length	Deletions	Inserts	Gaps
Matches 395; Conservative 0; Mismatches 73; Indels 0; gaps 0;	95.0%	351.7	455	65	0	0
QY 1 ATGGTCTGAGTGGGGCGCTGCTTCGAATGAGAAGCTCGCATGAAAGGTCTTAT 60						
Db 234 ATGGTCTGAGTGGGCACTATGCTTCGAATGAGAAGTCGCCTGAGGTCTAT 293						
QY 61 CTGCGATATAACCAGGCTCTAGCTGAGGGCTGATCGAGGAGTCATTAAGGTAA 120						
Db 294 CTGCGATATAACCAGGCTGCTGAGGACTGCAACAGAGAGTCATTAAAGTGAG 353						
QY 121 GAGATAGCGTGGTCCCCTAATGGTGGCTGGATGCCAGCCGTCCTCGTCACTGGT 180						
Db 354 GAGATAGCTGTCCTCAAATGGGACTGATGCCAGTCGTCCTCGTCACTGGC 413						
QY 181 GTCGACAGGGAGGCAGTGCCTGCTAGTGGGGTGGGGAGGGCGACTCTAACATA 240						
Db 414 GTCGAAGGAGGAGCACTGTCCTATCTGTGGGACAGAGAAGGGCAATTCTGAACCT 473						
QY 241 GAGCCAGTGAACATCTGGACCTCTTCTTGGTGCAGGAATCCAGAGCTCACCTTC 300						
Db 474 GAGCCAGTGAACATCTGGACCTCTTCTTGGTGCAGGAATCCAGAGCTCACCTTC 533						
QY 301 TACCGGGGGACATGGGGCTACCTCCAGCTTGGAGTGGGCTCCACCGGACTGGTC 360						
Db 534 TACCGGGGGATATGGGGCTTACCTCCAGCTTGGAGTGGGCTCCACCGGACTGGTC 593						
QY 361 CTCTGACGGTCTCTGAGGCGATCTACGGCTGTCAGACTACCCGCTTCGGAGATGGT 420						
Db 594 CTCTGACCTCACCGAGACTGACCTGTCAGCTCACTGAGATCCCTGAGGACCCC 653						
QY 421 GGTGGAATGCCCTACAGACTCTACTTCAGCGTGTGACTAG 468						
Db 654 GCCTGGGATGCTCCATCACAGACTCTACTTCAGCGTGTGACTAG 701						

DEFINITION	AGENCOURT 12780806 NIH MGC 136 <i>Mus musculus</i> cDNA clone IMAGE:30286859 5', mRNA sequence.	Qy	3 61 CTGAGCACGSGTGCTGAAGCCGATCAGCTGTCAGACTACCCAGCTCCGAGATGGT 420
ACCESSION	CB590160	D	4 45 CTCTCACCTCACCGGAAGCTGACCAGCTGTCAGCTACTCAGATCCTGAGGACCC 504
VERSION	CB590160.1	GI:	29508016
KEYWORDS			
SOURCE	<i>Mus musculus</i> (house mouse)	Qy	4 21 GGCCTGAAATCCCGATTCAGATTCCTACTTCAGCCAGCTGACTAG 468
ORGANISM		Db	5 05 GCCTGGATGCTCCATCACAGACTCTACTTCAGCAGTGACTAG 552
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Burchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov		
FEATURES	Tissue Procurement: Dr. David Rowe cDNA Library Preparation: Invitrogen Corp DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov		
SOURCE	Plate: NDAM21 row: m column: 12 High quality sequence stop: 576. Location/Qualifiers		
FEATURES	1. .862 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:30286859" /tissue_type="embryonic limb, maxilla and mandible" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_136" /note="vector: pCMV-SP6R6.1; Site 1: EcoRV; Site 2: NotI; Normalized, full-length enriched library from pool of mouse embryonic limb, maxilla and mandible, embryonic day 17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw equivalents from respective days). Cloned directionally, oligo-dT primed (5'-GACAGTCTAGATGGCGACGCCGCCC(R15-3'. Size selected for the >1kb fragments, average insert size 1.2 kb. Normalization to Cot 7.5. Tissue contributed by David Rowe; library constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	74.7%; Score 349.6; DB 6; Length 862;		
Best Local Similarity	84.2%; Pred. No. 1.1e-85;		
Matches	394; Conservative 0; Mismatches 74; Indels 0; Gaps 0;		
Qy	1 ATGGTCTCTGAGCTGGGGCGCTGTGCTCGGAATGAAAGACTGGCATGAAAGCTTAT 60		
Db	85 ATGGTCTCTGAGCTGGGAACATGCTTCGAAAGGATTAGCCTTGAAAGTACTGTAT 144		
Qy	61 CTGCAATATACCCAGCTCTGCTGGAGGTGATCGACCGAAAGCTTATTAAGGTGAA 120		
Db	145 CTGCACATATAACCCAGCTCTGGAGACTGAGCTGAGGAAAGGTATTAAGGTGAG 204		
ORIGIN			
Query Match	73.3%; Score 343.2; DB 6; Length 885;		
Best Local Similarity	83.3%; Pred. No. 6.6e-84;		
Matches	390; Conservative 0; Mismatches 78; Indels 0; Gaps 0;		
Qy	1 ATGGTCTCTGAGCTGGGGCGCTGTGCTCGGAATGAAAGACTGGCATGAAAGCTTAT 60		
Db	85 ATGGTCTCTGAGCTGGGAACATGCTTCGAAAGGATTAGCCTTGAAAGTACTGTAT 144		
Qy	61 CTGCAATATACCCAGCTCTGCTGGAGGTGATCGACCGAAAGCTTATTAAGGTGAA 120		
Db	145 CTGCACATATAACCCAGCTCTGGAGACTGAGCTGAGGAAAGGTATTAAGGTGAG 204		
Qy	121 GAGATCGCGCTGGTCCCAATGGTGTGATGCCAGCTGCTCCCGTGTATCTGGT 180		
Db	205 GAGATCGCTGGTCCCAATGGTGTGATGCCAGCTGCTCCCGTGTATCTGGT 264		
Qy	181 GTCGAGGGTGGAAAGCCAGTGGCTGTGATGCTGGGGCGGAGCTAACTA 240		
Db	265 GTCTCAAGGAGAGGACGCTTATCTGTGGAGACAGAGAAGGCCAATCTGAACCT 324		
Qy	241 GAGCCAGTGAACATCTGGAGCTCTCTGGCTGGAGGATCCAGAGTTACCTTC 300		
Db	325 GAGCCAGTGAACATCTGGAGACGCTTACCTCTGGGGCAAGGATCAAGGTTACCTTC 384		
Qy	301 TACCGGGGGACATGGGGCTCTCTGGCTGGAGCTGGCTACCCGGCTGGTC 360		
Db	385 TACCGGGGGATGGGCTTACCTCTGGCTGGAGCTGGCTACCCGGCTGGTC 444		

LOCUS BY09379 **708 bp** **mRNA** **linear** **EST** **16-DEC-2002**
DEFINITION BY09379 RIKEN full-length enriched, adult male tongue Mus musculus
CDNA CLONE 230041K075, mRNA sequence.

VERSION BY093779.1 GI:27120580
KEYWORDS EST.
SOURCE MUS MUSCULUS (house mouse)
ORGANISM MUS MUSCULUS

Kiyobawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanpin, A., Matsuda, H.,

Chotnia, C., Corrall, L. B., Cousins, S., DeJarnett, J. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaaster, T., Fletcher, C. F., Forrester, A., Frazer, K. S., Gaaster, T., Garibaldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guarnaccia, S., Hirokawa, N., Jackson, J., Jarvis, E. D., Kanai, A.,

Kurohkin, I. V., Lee, Y., Lemhard, B., Lyons, P. R., Maglott, D. R., Maltsev, L., Marchionni, M., McKenzie, L., Miki, T., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pessole, L.,

Ravasi, T., Reed, J.C., Reed, D.J., Read, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, R., Setou, M., Shimada, K.W., Sultana, R., Takeuchi, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Ueda, R., Whibley, C., Yano, T., Yawata, Y., Yamada, Y., Yamane, T.

Wells, C., Wiliams, D., Wu, J., Xiang, J., Xiong, J., Yang, J., Yuan, Z., Zavoli, M., Zhu, Y., Zimmer, A., Carrin, M., Hayashi, N., Hizukuri-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shikata, T., Wakiki, H., Nakajima, J., Alzawa, K.,

ITO, M., KAGAWA, I., MIYAZAKI, A., SAKAI, K., SASAKI, D., SHIBATE, K., SHINGAWA, A., YASUNISHI, A., YOSHINO, M., WATERSTON, R., LANDER, E.S., ROGERS, J., BIRNEY, E., AND HAYASIZAKI, Y.

JOURNAL Nature 420, 563-573 (2002)
PUBLISHED 1246851
COMMENT <http://www.genome.jp/kegg/entry/1246851>
Contact: Yoshihide Hayashizaki
Human Genome Research Research Group, RIKEN Genomic

Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@qsc.riken.jp, URL:<http://genome.qsc.riken.jp/>

ORIGIN NIH."

QY 241 GACCCAGTGACATCATGGGCTCTATCTGGTCCAAAGGAATCCAAAGAGCTCACCTC 300

Db 473 GAGCCAGTGACATCATGGGCTCTATCTGGTCCAAAGGAATCCAAAGAGCTCACCTC 532

QY 301 TACGGGGGGGACATGGGCTCTACCTCCAGTGGCTGAGTCAGTCAGCTGGCTCCTACCCGGCTGGTC 360

Db 533 TACGGGGGGGACATGGGCTCTACCTCCAGTGGCTGAGTCAGTCAGCTGGCTCCTACCCGGCTGGTC 592

QY 361 CTCGACGGTGCCTGAAGCCGATCAGCTGTGAGCTACCCAGCTCCCGAAGATGTT 420

Db 593 CTCGACCTCACCGGAAGCTGACCGCTGTCAGGCTCACAGAACCTGGAGACCC 652

QY 421 GGCTGGAAATGCCCATCACAGACTCTACTCCAGCAGTGTACTAG 468

Db 653 GCCTGGGATGTCATCACAACTTTACTTTAACCTTAAGCATGTGACTAG 700

RESULT 15

CR42272

DEFINITION CR42272 Soares_parathyroid tumor NbHPA Homo sapiens mRNA linear EST 21-DEC-2004

ACCESSION IMAGE:1647934

VERSION CR42272

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E.,

TITLE I.M.A.G.E. cDNA Clone Collection

JOURNAL Unpublished (2004)

COMMENT Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD; IMAGE:1647934

RZPD; I.M.A.G.E. cDNA Clone Collection;

Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD: contact RZPD (clone@rzpd.de) for further information. Seq primer: MIJU. Primer sequence: CGTTGAAACGACGGCCAGT.

FEATURES

source

1. 414

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1647934"

/tissue_type="parathyroid tumor"

/dev_stage="adult"

/lab_host="DHB10B (ampicillin resistant)"

/clone="Soares parathyroid tumor NbHPA"

/note="Organ: parathyroid gland; Vector: pRT3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

/lab="DHB10B (ampicillin resistant) clone" "Soares parathyroid tumor NbHPA"

This clone was selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3D vector (Pharmacia). Library went through one round of normalization to a C_{ot} = 5. Library constructed by Bentol Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, Institute of Diabetes and Digestive and Kidney Diseases,

RESULT 16

AK01020

DEFINITION AK01020 Mus musculus adult male tongue cDNA. RIKEN full-length enriched library, clone:2310063B08 product: interleukin 1 family, member 5 (delta), full insert sequence.

ACCESSION AK01020

VERSION AK01020.1 GI:12845175

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol.

PUBMED 1049636

REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, R., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res.

PUBMED 11042159

REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hayada, A., Yamamoto, R., Matsuno, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res.

PUBMED 11076861

REFERENCE

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Db	1	AATGAAAGGATTAGCCCTGAGGTTACTGTATCTGCACATAACCAAGCTGCTGCTGGAGG	60	CDNA-collection"
Qy	90	GETGCACTGCAAGGAAGCTCACTAAGTTGAGAGATCAGCCGTTGCCATCGGAGCT	149	ORIGIN
Db	61	ACTGCACTGCAAGGAAGCTCACTAAGTTGAGAGATCAGCCGTTGCCATCGGAGCT	120	Query Match
Qy	150	GGATGCCAGCTGTCCTCCCGTCACTCTGGTGTCCAGGGTGGAGCCATGCTGTGATG	209	57.9%; Score 271; DB 5; Length 338;
Db	121	GGATGCCAGCTGTCCTCCCGTCACTCTGGTGTCCAGGGTGGAGCCATGCTGTGATG	180	Best Local Similarity
Qy	210	TGGGTTGGGAGGAGGCCATCACTAGAGCCAGTCAAGCTAAGCTAGGAGCTCTATCT	269	100.0%; Pred. No. 5.6e-64;
Db	181	TGGGACAGAGAAGGAAATCTGAACTTGAGGAGCTGACATCGAGCTCTACTT	240	Mismatches
Qy	270	TGGTGCCTAGGAAATCCAGAGCTCACTTCTACCGCGGACATCGGCTCACCTCGAG	329	271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	241	CGGGCCAGGAAATCAAGAGCTCACCTTCTACCGGGAGATATGGCTTACCTCGAG	300	Matches
Qy	330	CTTCGAGTCGGCTGCCCTACCCGGCTGGTCTCTGTGACCGCTCTGAGCCATGCC	389	1 ATGGTCTTGAGTGGGGCTGTCCTCGAAGGAGCTGCTGCTGAAATGAGGTCTTAT
Db	301	CTTCGAAATCCGCTGCCCTACCCGGCTGGTCTCTGTGACCTCACCGAGCTGACGCC	360	68 ATGGTCTTGAGTGGGGCTGTCCTCGAAGGAGCTGCTGCTGAAATGAGGTCTTAT
Qy	390	TGTCAGACTCACCAGCTCCCGAGAATGGTGGCTGGATGCCATCACAGACTCTA	449	127
Db	361	TCTCAGCTCTACTCGAGGACCCGCCCTGGATGCTCCCATCACAGACTCTA	420	61 CTGCATATAACCAAGCTCTACGCTGAGGAGCTTAAAGTGA
Qy	450	CTTCAGCAGCTGACTAG	468	120
Db	421	CTTCAGCAGCTGACTAG	439	128 CTGCATATAACCAAGCTCTACGCTGAGGAGCTTAAAGTGA
<hr/>				
RESULT 18				
LOCUS	BX477358	338 bp	mRNA	linear EST 04-SEP-2003
DEFINITION	DKRZP686022193 r1 686 (synonym: h1cc3)	Homo sapiens	CDNA clone	
ACCESSION	BX477358			
VERSION	DKRZP686022193 5'			
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.			
TITLE	1 (bases 1 to 338)			
JOURNAL	Anorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Weil, B., Anide, C., Robo, G., Han, M. and Wiemann, S.			
COMMENT	EST (Anorge, W., Krieger, S., Regiert, T., Rittmueller, C., et al.)			
<hr/>				
RESULT 19				
LOCUS	CB194288	898 bp	mRNA	linear EST 05-FEB-2003
DEFINITION	AGENCOURT 11259798 NIH MGC 135 Mus musculus cDNA clone			
ACCESSION	CB194288			
VERSION	CB194288.1			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glirs; Rodentia; Sciuromorphi; Murodoidea; Muridae; Murinae; Mus.			
REFERENCE				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgraphs-r@mail.nih.gov			
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				
Source				
<hr/>				
FEATURES				

QY	128	GGCTGGTCCCCATCGCTGGCTGATGCCAGCTGTGCCCCCATCGCTGGCTGAGG 187	Sciences Center(GSC), Yokohama Institute
Db	1	GTTGTGCCCCATCGGCACTGGCTGATGCCAGCTGTGCCCCCATCGCTGGCTGAGG 60	The Institute of Physical and Chemical Research (RIKEN)
QY	188	GGGAGGCACTGGCTGATGCCAGCTGTGCCCCCATCGCTGGCTGAGG 60	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Db	61	GGGAGGCACTGGCTGATGCCAGCTGTGCCCCCATCGCTGGCTGAGG 60	Tel: 81-45-503-9222
QY	248	TCACATCATGGACTCTATCTGGCTGAGGATCCAGGCTCACCTCTACCGCAG 247	Fax: 81-45-503-9216
Db	121	TGACATCATGGACTCTATCTGGCTGAGGATCCAGGCTCACCTCTACCGCAG 180	Email: genome-reseqc.riken.jp, URL: http://genome.gsc.riken.jp/
QY	308	GGGACATGGGGCTACCTCCAGTCAGTCGGCTGCTACTCCGGCTGGTCTGCA 367	Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Ciminci,P.,
Db	181	GGGATATGGCTTACCTCCAGCTGGCTGCTACCCAGGTGGTCTCTGCA 240	Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
QY	368	CGGTGCTGAAGCCGATCTACCTGGCTGAGCTACCCAGCTGGTCCGAGA 427	Imatori,K., Ishii,Y., Itoh,M., Kawagawa,I., Kawai,J., Kojima,Y.,
Db	241	CCTCACCGGAAGCTGACCAGGCTGAGGTCTACCTGAGATGGTGGTGA 300	Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
QY	428	ATGCCCATACAGACTCTACAGCTTCAAGCTGAGCTGACTAG 468	Nomura,K., Numazaki,R., Ohno,M., Ohbayo,N., Saito,R., Sakazume,N.,
Db	301	ATGCTCCATACAGCTTCAAGCTGAGCTGACTAG 341	Sano-H., Sabaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watanuki,A., Muramatsu,M. and Hayashizaki,Y.
RESULT 21			
BY708859	BY708859	686 bp mRNA linear EST 16-DEC-2002	Direct Submission
DEFINITION	BY708859	musculus cDNA clone 2210418104 5', mRNA sequence.	Computational Analysis of Full-Length Mouse cDNAs Compared with
ACCESSION	BY708859	BY708859.1 GI:27120053	Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
VERSION			Normalization and subtraction of cap-trapper-selected cDNAs to
KEYWORDS			prepare full-length cDNA libraries for rapid discovery of new
EST.			genes. Genome Res. 10 (10), 1617-1630 (2000)
SOURCE	Mus musculus (house mouse)		RIKEN integrated sequence analysis (RISA) system-384-format
ORGANISM	Mus musculus		sequencing pipeline with 384 multicapillary sequencer. Genome Res.
REFERENCE	Bulkyoya, Motzora; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Eutherioniglires; Glirida; Rodentia; Sciurognathi; Muridae; Murida; Murinae; Mus.		10 (11), 175-171 (2000)
AUTHORS	1 (bases 1 to 686)		Computer-based methods for the mouse full-length cDNA
	Kijosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nagami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Built,C., Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Niiyama,I., Otao,N., Saito,R., Suzuki,H., Yamamoto,I., Kijosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nagami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Built,C., Hune,D.A., Chackenbush,J., Schrimpf,L.M., Kanapin,A., Matsuda,H., Balalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Ciochta,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.P., Forrest,A., Frazer,K.S., Gaasterland,T.A., Garibaldi,M., Gissel,C., Godzik,A., Gough,J., Grifmondo,S., Guatincicich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konayaya,A., Kurochkin,I.V., Lee,Y., Lenhoff,B., Lyons,P.A., Maglott,D.R., Maitrais,L., Marchionni,L., McKenize,L., Miki,H., Nagashima,T., Numata,K., Orido,T., Pavan,W.J., Pertea,G., Persole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ringwald,M., Sandelin,A., Schneider,C.A., Semple,C., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Weil,C., Winnik,L.G., Wynnhab-Horis,A., Yanagisawa,M., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kondo,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Ichii,M., Kageyama,I., Mizazaki,A., Sakai,D., Shibata,K., Shinagawa,A., Yashida,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.	encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	
FEATURES	source		cDNA library was prepared and sequenced in Mouse Genome
			Encyclopedia Project of Genome Exploration Research Group in Riken
			Genomic Sciences Center and Genome Science Laboratory in RIKEN
			Division of Experimental Animal Research in Riken contributed to
			Please visit our web site (http://genome.gsc.riken.go.jp) for
			further details.
			Location/Qualifiers
			1. 686
			/organism="Mus musculus"
			/mol_type="mRNA"
			/db_xref="taxon:10990"
			/clone="2210418104"
			/sex="male"
			/tissue_type="stomach"
			/dev_stage="adult"
			/lab_host="SOIR"
			/clone_id="RIKEN full-length enriched, adult male
			/stomach"
			/note="Site 1: XhoI, Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGCGCCGCACTGAGTTTTTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTGAGTTTAATTAATCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI."
			ORIGIN
			Query Match
			51.0%; Score 238.8; DB 5; length 686;
			Best Local Similarity 82.1%; Pred. No. 5; 4e-5;
			Matches 299; Conservative 0; Mismatches 62; Indels 3; Gaps 2;
QY	1	ATGGTCCTGAGTGGGGCTGCTCGAATGAAGGACTCGATGAGGTGCTTAT 60	
Db	133	ATGGTCCTGAGTGGGGCTGCTCGAATGAAGGACTCGATGAGGTGCTTAT 192	
QY	61	CTGCATATAACCAGCTCTAGCTGGGGCTGCTCGAATGAAGGTGA 120	
Db	193	CTGCACATACACGCTGCTGAGCTGAGGTGCTTACAGGAGGTCAATTAGGTGAG 252	
COMMENT	Contact: Yoshihide Hayashizaki		Laboratory for Genome Exploration Research Group, RIKEN Genomic

COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shiraki, T., Tagami, M., Waki, K., Watanuki, A., Muramatsu, M. and Hawashizaki, Y. Direct Submission RIKEN Integrated Analysis of Full-Length Mouse cDNA Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedias: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	
FEATURES	source	
ORIGIN	1. 348 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref=taxon:10930" /clone=L330027819" /tissue_type="whole body" /dev_stage="15 days embryo" /clone lib="RIKEN full-length enriched, 15 days embryo whole body"	
KEYWORDS	EST. Mus musculus (house mouse)	
SOURCE	Mus musculus	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murine; Mus.	
REFERENCE	1 (bases 1 to 343) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Konno, S., Okaido, I., Otao, N., Saito, R., Suzuki, H., Yamamoto, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nagami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Built, C., Hume, D.A., Okamoto, S., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Dragani, T.A., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dill, D., Dragan, T., Fletcher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gibbs, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirakawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kishimura, R., Konagaya, Y., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Naglott, D.R., Maltais, J., Marchlinski, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavani, W.J., Pertea, G., Peso, E.G., Petrovsky, N., Pilai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneide, C., Sepulveda, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L., Wynn-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane, K., Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kaga, T., Miyazaki, A., Sakai, K., Sasaki, D., Shikata, K., Rogers, J., Birney, B. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002) Nature 420, 563-573 (2002) 1246851	
JOURNAL	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanuki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedias: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	
COMMENT	source	
TITLE	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanuki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedias: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	
FEATURES	source	
RESULT	24	
BY10750	343 bp mRNA linear EST 07-DEC-2002	
LOCUS	BY10750 RIKEN full-length enriched, 15 days embryo whole body Mus musculus cDNA clone L330014H07 5', mRNA sequence.	
DEFINITION	BY10750	
ACCESSION	BY10750	
VERSION	BY10750.1 GI:26218367	

ORIGIN

Query Match 34.5%; Score 161.6; DB 5; Length 343;
Best Local Similarity 86.1%; Pred. No. 1.2e-33; Mismatches 29; Indels 0; Gaps 0;
Matches 179; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGTCTCTGAGTGGGGCTGCTGCGTGAAGGACTGGATGAAAGGTATT 60
Db 136 ATGGTCTGACTGGGCACTATGCTTCCGAATGAAGGATTAAGCTGAAGGTACTGTAT 195

QY 61 CTGCACTATAACCAGCTCTAGCTGGAGGGTGCATGCAGGGCTTAAAGTGAA 120
Db 196 CTGCACTATAACCAGCTCTAGCTGGAGGGTGCATGCAGGGCTTAAAGTGAA 255

QY 121 GAGATAGCGGTGCTCCAACTGGTCACTGCGCTGAGGAGTCAGTAAAGTGAC 180
Db 256 GAGATAGCGGTGCTCCAACTGGTCACTGCGCTGAGGAGTCAGTAAAGTGAC 315

QY 181 GTCCAGGGTGAAGCCGTGCTGTCA 208
Db 316 GTCAGGAGGAGAGCCGTGCTATCT 343

RESULT 25

LOCUS CK947864 DEFINITION CK947864 689 bp mRNA linear EST 15-MAR-2004
ACCESSION CK947864 VERSION CK947864.1 KEYWORDS EST.
SOURCE Bos taurus (cow)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 689)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bokak, S., Rubenfield, M. and Gassbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically activated bovine gut
JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt " -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 12
Plate: 25 row: A column: 09
Seq primer: CCCAGTCAGCACCGTGTAAACCG
High quality sequence stop: 689.

FEATURES source

1. .689

/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="10BOV23_A09"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"

ORIGIN

Query Match 34.2%; Score 160; DB 7; Length 689;
Best Local Similarity 76.6%; Pred. No. 3.7e-33; Mismatches 60; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 213 GGTGGGGAGAGCGACATCAACCTCTAGCTAGCCAGTCATCGGCTCTCTGG 272
Db 172 GGAGGCCATACAGCGGGGAAGGTCAATTAAAGCTGACATGAGCTTACACAG 231

QY 273 TGCCAAAGGAATCCAAAGGCCTCACCTCTACCGGGGACATGGGGCTCACCTCAG CTT 332
Db 232 TGCCAAAGGAATCTAAAAATCACTTCTACCGGGGACACGGGGCTCACCTCAG CTT 291

QY 333 CGAGTCGCTGCTAACCGGGCTGTTCTGTGAAGGCTGTAGCCATCAGGGT 392
Db 292 TGAGTGGCTCTAACCGGGCTGTTCTGTGAAGGCTGTAGCCATCAGGGT 351

QY 393 CAGACTAACCCAGCTTCCGAGAATGTGTSCTGGATGCCCATCACAGCTCTCATTT 452
Db 352 GCAGATACCCAACTCCGGAGGACACAGCTGGGACACCCATCATCGACTCTCATTT 411

QY 453 CCAGCAGTGTGACTAG 468
Db 412 CCAGCAGATGTGACTAG 427

RESULT 26

LOCUS CK952430 DEFINITION CK952430 702 bp mRNA linear EST 15-MAR-2004
ACCESSION CK952430 VERSION CK952430.1 KEYWORDS EST.
SOURCE Bos taurus (cow)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 702)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bokak, S., Rubenfield, M. and Gassbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically activated bovine gut
JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt " -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 12
Plate: 25 row: L column: 23
Seq primer: CCCAGTCAGCACCGTGTAAACCG
High quality sequence stop: 702.

FEATURES source

1. .702

/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="10BOV23_A09"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"

ORIGIN

/lab_host="DH10B TI phage resistant"
/clone lib=BARC 10BOV"
/note="organ: Small Intestine; Vector: pAgen-1; Site 1: BovIV; Site 2: NotI; Equimolar amounts of mRNA extracted from proximal jejunums of 18 and 21 wk old steers, and distal ileums of 14 day old calves. proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"

QY 1 (bases 1 to 702)
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"

ORIGIN

Query Match 34.2%; Score 160; DB 7; Length 702;
Best Local Similarity 76.6%; Pred. No. 3 8e-33;
Matches 196; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
/lab_host="DH10B TI phage resistant"
/clone_lib="BAC 1030V"
/note="Organ: Small Intestine; Vector: pagen-1; site_1:
ECOR1; Site_2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunum of 1 day old calves: proximal jejunum
exposed to C. oncophara for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

RESULT 27

CD568042/c

LOCUS CD568042 689 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FTI-bkc-a-09-0-UI_81 NCI_CGAP_FTI Homo sapiens cDNA clone
ACCESSION CD568042
VERSION 1. GI:31152132
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Cetartiodactyla;
Hominoidea; Homo.
1 (bases 1 to 689)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Title Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiova.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
Sequence: 31-139, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLY(A) Yes.

FEATURES

source 1. . 689 Location/Qualifier
/organism="Homo sapiens"
/mol_type="mRNA"

ORIGIN

Query Match 34.2%; Score 160; DB 7; Length 702;
Best Local Similarity 76.6%; Pred. No. 3 8e-33;
Matches 196; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
/lab_host="DH10B TI phage resistant"
/clone_lib="BAC 1030V"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: ECOR 1; Site 2: Not 1;
NCI_CGAP_FTI is a normalized cDNA library constructed from
a Pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Klebsiella
PVA 10 ng/ml, 3 hours; PVA 10 ng/ml, 24 hours; Klebsiella
mvi 10, 3 hours; Klebsiella mvi 10, 24 hours; Staph aureus
mvi 10, 3 hours; Staph aureus mvi 10, 24 hours; Adenoviral vector
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1995. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not 1 site.
Double stranded cDNA was ligated to an ECOR 1 adaptor,
digested with Not 1, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first strand cDNA contains a library tag
sequence that is located between the Not 1 site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCC. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GCCATGCC"

ORIGIN

Query Match 32.7%; Score 153; DB 6; Length 689;
Best Local Similarity 100.0%; Pred. No. 3 3e-31;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/lab_host="DH10B TI phage resistant"
/clone_lib="BAC 1030V"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: ECOR 1; Site 2: Not 1;
NCI_CGAP_FTI is a normalized cDNA library constructed from
a Pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Klebsiella
PVA 10 ng/ml, 3 hours; PVA 10 ng/ml, 24 hours; Klebsiella
mvi 10, 3 hours; Klebsiella mvi 10, 24 hours; Staph aureus
mvi 10, 3 hours; Staph aureus mvi 10, 24 hours; Adenoviral vector
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1995. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not 1 site.
Double stranded cDNA was ligated to an ECOR 1 adaptor,
digested with Not 1, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first strand cDNA contains a library tag
sequence that is located between the Not 1 site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCC. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GCCATGCC"

RESULT 28

CC526753

LOCUS CC526753 784 bp DNA linear GSS 17-JUN-2003
DEFINITION CH240_401P1.T7 CHORI-240 Bos taurus genomic clone CH240_401P1,
genomic survey sequence.
ACCESSION CC526753
VERSION CC526753.1 GI:31845041
KEYWORDS GSS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 784)

REFERENCE

AUTHORS	Holt, R., Stott, J., Yang, G., Barber, S., Smallis, D., Prabhu, A.-L., Teai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Mathewson, C., Wye, N., Masson, A., Brown, John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J.-W., and Kappes, S. M.
REFERENCE	1 (bases 1 to 501)
AUTHORS	Adelson, D. L., Cam, G. R., Desilva, U. and Franklin, I. R.
TITLE	Gene expression in sheep skin and wool (hair)
COMMENT	Genomics 83 (1), 91-105 (2003)
JOURNAL	Unpublished (2003)
COMMENT	Other GSBS: CH240_401P1.TARBC13P2
CONTACT	Contact: Rob Holt
SEQUENCING	Sequencing
THE BRITISH COLUMBIA CANCER AGENCY GENOME SCIENCE CENTRE	The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6	600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
TEL:	604-877-6285
FAX:	604-877-6276
EMAIL:	rhol@bccgbc.ca
CLONES	Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdj@jong@mail.cho.org).
COMMENT	Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering-information.html). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
SEQUENCING	Seq primer: T7
FEATURES	Location/Qualifiers
SOURCE	Class: BAC ends.
1. .784	1. .784
/organism="Bos taurus"	/organism="Bos taurus"
/mol_type="genomic DNA"	/mol_type="genomic DNA"
/strain="Breed: Hereford"	/strain="Breed: Hereford"
/clone="CH240_401P1"	/clone="CH240_401P1"
/db_xref="taxon:9913"	/db_xref="taxon:9913"
/sex="Male"	/sex="Male"
/cell_type="Blood"	/cell_type="Blood"
/clone_libr="CHORI-240"	/clone_libr="CHORI-240"
/note="Vector: pTARRAC1_3; Site_1: MboI; Site_2: MboI; Hereford bull Li Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"	/note="Vector: pTARRAC1_3; Site_1: MboI; Site_2: MboI; Hereford bull Li Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
ORIGIN	ORIGIN
QUERY	Query Match 28.0%; Score 131; DB 9; Length 784; Best Local Similarity 78.2%; Pred. No. 4; 6e-23; Matches 169; Conservative 0; Mismatches 46; Indels 1; Gaps 1;
DB	Query Match 26.8%; Score 125.2; DB 6; Length 501; Best Local Similarity 60.9%; Pred. No. 1; 6e-23; Matches 240; Conservative 0; Mismatches 148; Indels 6; Gaps 2;
QY	15 GCGCTGCTTCGAATGAGACTCGCGATTAAGGTCTTATCGATATAACCA 74
DB	69 GCGAAATACTACTATAATTAAAGATGAGAGAGAGAGATCGGGT 128
QY	75 GCTCTAGCTGGAGGCTGTCAGCAGGGAGGTCTAAAGGTGAGAGATCGGGT 134
DB	129 GTCCTGGGGAGATCCGATCAGACAA---CTGCTGAGAGACCATCTGCAT 185
QY	135 CCCAATGGTGGCTGGATGCCGCCTCTCCCGCTCATCTCTGGTGGAGG 194
DB	246 CCCATGGCTGGATCTGGTGGAGACAGGGGGGGCTCTCAGTGAGATGAA 305
QY	186 CCCAACAGAGACCTGGACGACCGACAGTCCTCTCTGGGGTCAGGGAGTAG 245
DB	195 CGCTGGCTGCTGCTGGGGTG---GGGAGAGGCCACTCTAACCTAGAGCGAGTGA 251
QY	245 CCCATGGCTGGATCTGGTGGAGACAGGGGGGGCTCTCAGTGAGATGAA 305
DB	252 CATCTGGAGCTATCTGGCGCAAGGATCAAGAGCTTACCTTACCCGGGGGA 311
QY	306 CATTGGAGCTTACAGGGTGAGAGAAACACCGCTTACCTTCTTCAGAGAAG 365
DB	312 CATTGGGCTACCTTCAGCTTCAGTCGCTGCCTACCGGGCTGGTCTGTGACGGT 371
QY	366 CTAGGCCGCTTCAGCTCCAGCTGCTGGTCTCTGGCT 425
DB	372 GCTGAAACGCCGATCAGCCGCTGCAAGTCACCCAG 405
QY	426 CTCGAAACCCACGCCCTGGCACTTACCAAG 459
RESULT 29	RESULT 29
CP116914	CP116914
OCUS	501 bp mRNA linear EST 23-JUL-2003
DEFINITION	adult sheep skin library Ovis aries cDNA, mRNA sequence.
VERSION	ad97.21
ACCESSION	CF116914
KEYWORDS	EST.
ORGANISM	Ovis aries (sheep)
RESULT 30	RESULT 30
CP116914.1	CP116914.1
DEFINITION	621 bp mRNA linear EST 17-DEC-2002
LOCUS	BY714015
DEFINITION	BY714015 RIKEN full-length enriched, 0 day neonate skin Mus
ACCESSION	BY714015
VERSION	musculus cDNA clone 4632413N13 5', mRNA sequence.
ACCESSION	BY714015.1
VERSION	GI:27126185
REFERENCE	Pecora, Bovidae; Caprinae; Ovis.
AUTHORS	1 Adelson, D. L., Cam, G. R., Desilva, U. and Franklin, I. R.
TITLE	Gene expression in sheep skin and wool (hair)
COMMENT	Genomics 83 (1), 91-105 (2003)
CONTACT	Contact: Adelson, David L.
THE CSIRO LIVESTOCK INDUSTRIES	CSIRO Livestock Industries
COMMENT	306 Carmody Road, St Lucia QLD 4067, Australia
CONTACT	Tel: +61 7 3214 2700
COMMENT	Fax: +61 7 3214 2900
EMAIL	1-enquiries@csiro.au.
FEATURES	Location/Qualifiers
SOURCE	1. .501
/organism="Ovis aries"	/organism="Ovis aries"
/mol_type="mRNA"	/mol_type="mRNA"
/strain="Merino"	/strain="Merino"
/db_xref="taxon:9940"	/db_xref="taxon:9940"
/sex="male"	/sex="male"
/dev_stage="Adult"	/dev_stage="Adult"
/lab_host="BM25.8"	/lab_host="BM25.8"
/clone_libr="ad adult sheep skin library"	/clone_libr="ad adult sheep skin library"
/note="Organ: midflank skin; Vector: pTRIPLEX; Site_1: EcoRI; Site_2: XbaI; Arranged library filters screened by hybridization with labeled dinucleotide repeats. First strand synthesis XbaI - dT15 primed. EcoRI adaptors were ligated to cDNA before cloning. EcoRI - NotI - Sall adaptor sequence: 5'-AATTCGGCCGCGCGAC 5', TCCGAGATCTGACGCCG 3', sequencing primer 5', TAACTGACTCTACATAGGG 3', submitted sequences in excess of 50 bp after vector and quality clipping(phred 13) submitted to GenBank."	/note="Organ: midflank skin; Vector: pTRIPLEX; Site_1: EcoRI; Site_2: XbaI; Arranged library filters screened by hybridization with labeled dinucleotide repeats. First strand synthesis XbaI - dT15 primed. EcoRI adaptors were ligated to cDNA before cloning. EcoRI - NotI - Sall adaptor sequence: 5'-AATTCGGCCGCGCGAC 5', TCCGAGATCTGACGCCG 3', sequencing primer 5', TAACTGACTCTACATAGGG 3', submitted sequences in excess of 50 bp after vector and quality clipping(phred 13) submitted to GenBank."
ORIGIN	ORIGIN
QUERY	Query Match 26.8%; Score 125.2; DB 6; Length 501; Best Local Similarity 60.9%; Pred. No. 1; 6e-23; Matches 240; Conservative 0; Mismatches 148; Indels 6; Gaps 2;
DB	Query Match 26.8%; Score 125.2; DB 6; Length 501; Best Local Similarity 60.9%; Pred. No. 1; 6e-23; Matches 240; Conservative 0; Mismatches 148; Indels 6; Gaps 2;
QY	15 GCGCTGCTTCGAATGAGACTCGCGATTAAGGTCTTATCGATATAACCA 74
DB	69 GCGAAATACTACTATAATTAAAGATGAGAGAGAGATCGGGT 128
QY	75 GCTCTAGCTGGAGGCTGTCAGCAGGGAGGTCTAAAGGTGAGAGATCGGGT 134
DB	129 GTCCTGGGGAGATCCGATCAGACAA---CTGCTGAGAGACCATCTGCAT 185
QY	135 CCCAATGGTGGCTGGATGCCGCCTCTCCCGCTCATCTCTGGTGGAGG 194
DB	246 CCCATGGCTGGATCTGGTGGAGACAGGGGGGGCTCTCAGTGAGATGAA 305
QY	186 CCCAACAGAGACCTGGACGACCGACAGTCCTCTGGGGTCAGGGAGTAG 245
DB	195 CGCTGGCTGCTGCTGGGGTG---GGGAGAGGCCACTCTAACCTAGAGCGAGTGA 251
QY	245 CCCATGGCTGGATCTGGTGGAGACAGGGGGGGCTCTCAGTGAGATGAA 305
DB	252 CATCTGGAGCTATCTGGCGCAAGGATCAAGAGCTTACCTTACCCGGGGGA 311
QY	306 CATTGGAGCTTACAGGGTGAGAGAAACACCGCTTACCTTCTTCAGAGAAG 365
DB	312 CATTGGGCTACCTTCAGCTTCAGTCGCTGCCTACCGGGCTGGTCTGTGACGGT 371
QY	366 CTAGGCCGCTTCAGCTCCAGCTGCTGGTCTCTGGCT 425
DB	372 GCTGAAACGCCGATCAGCCGCTGCAAGTCACCCAG 405
QY	426 CTCGAAACCCACGCCCTGGCACTTACCAAG 459

FEATURES	division	of Invitrogen.
FEATURES	source	Location/Qualifiers
FEATURES	source	1. .884
FEATURES	source	/organism="Homo sapiens"
FEATURES	source	/mol_type="mRNA"
FEATURES	source	/db_xref="taxon:9606"
FEATURES	source	/tissue_type="normal nasopharynx"
FEATURES	source	/clone_lib="homo sapiens PLACENTA"
FEATURES	source	/note="ECRs generated from a normal nasopharynx cDNA library from southern Chinese"
ORIGIN		
Query Match		23.9%; Score 111.9; DB 6; Length 593;
Best Local Similarity		59.1%; Pred. No. 8.3e-20;
Matches		238; Conservative 0; Mismatches 147; Indels 18; Gaps 2;
Qy		24 CTTCCGATGAGGAGCTGGATTGAGGGCTTATCTGGATAATAACCGCTTCTAGC 83
Db		141 CTTCAGAATCTGGGACTTAAACAGAGACTCTATCTGGGAGAACCCACTAGTGC 200
Qy		84 TGGAGGCTGTGAGGAGGAGTCATAAGGTGAGAGTCAGCGTGTGTCATCG 143
Db		201 TGGATACCTGAGGACCAATTCAGAAGAGATAGTGGTACCCATG 260
Qy		144 GTCGCTGATGTCAGCCAGCTCTGGTGGCTGAGACAGCTCCAGCTGGAGGAGCTG 203
Db		261 GCCTCATGCTC-----TGTTCCTGGGATCCATGTGGAGGAGATGTCCT 305
Qy		204 GTCATGGGGTGGGTC-----GGCGAGGCGACTCTAACCTAGGCCACTGAACATCTGG 260
Db		306 GTCCTGTCAGTCAGTCAGTGGAGACAGCTCCAGCTGGAGGAGCTG 365
Qy		261 GCTCTATCTGGTGGCAAGGAATCCAGAGCTCTACCTCTACCCGGGAGCATGGCT 320
Db		366 CCTGAGGAGAACAGAAGCCTGCTGCTGAGGAGGAGGCC 425
Qy		321 CACCTCCAGCTTCAGTGGCTACCGCGCTGGTCTGTGAGCGGCTGAGC 380
Db		426 CACCACTGGTTCTGAGCTGGCCGCTGCCGCTGGTCTCTGCACAGGGATGGAGC 485
Qy		381 CGATCAGCTGTGAGACTCACCCAGCTCCCGAGATGGTGC 423
Db		486 TGACCAAGCCGTCAGCCTCACCAATATGGCTGACGAAGGCC 528
RESULT 32		
BX416942		
LOCUS		BX416942 884 bp mRNA linear EST 03-MAY-2004
DEFINITION		884 bp mRNA linear EST 03-MAY-2004
ACCESSION		CSODE001YA18
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
Genoscope - Centre National de Sequencing		
1 (bases 1 to 884)		
Li, W.B., Gruber, C., Jesse, J. and Polaves, D.		
Full-length cDNA libraries and normalization		
Unpublished (2001)		
On May 15, 2003 this sequence version replaced gi:30763662.		
1 (bases 1 to 470)		
Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J., Adams, M.D. and Cargill, M.		
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
Science 302 (5652), 1960-1963 (2003)		
2 (bases 1 to 470)		
Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,		

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zhong, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES

source

1. 470
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="Taxon: 9606"
 <1. .>470
 /gene="ILRN"
 /locus_tag="HCM1393"

ORIGIN

Query Match 23.5%; Score 110.2; DB 10; Length 470;
 Best Local Similarity 58.8%; Pred. No. 2.2e-19;
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

Qy 24 CTTCCGATGAGGAGCTGGCATGAAAGGTCTTATCTGCTATAAACGCTCTAGC 83
 Db 47 CTCAGAACTGGATGTTAACAGAGACCTCTATCTGCTATAAACGCTCTAGC 106
 Qy 84 TCGAGGGCTGCATGCAGGGAGGCTATTAAGGTGAGAGATCAGCTGGTGGCCCATCG 143
 Db 107 TGGATACGTGAGGACAAATCTCAATTAGAGAAAGATAGATGTTGAGACCCATGA 166
 Qy 144 GTCGCTGATGCCAGCCATCTGGGTCATCTGGGTCAGGGTGGAAACCCAGTCCT 203
 Db 167 GCTCTCATGCTC-----TGTCTTGGTAACTCATGAGGGAAATGTCCT 211

Qy 204 GTCATGTTGGTGTGAGGAGGACTCTAACATAAGCCAGTCTGAACATCATGGA 260
 Db 212 GTCCTGTCAGTCTGGTGTGAGGAGGACTCTAACATAAGCCAGTCTGAACATCATGGA 271

Qy 261 GTCCTATCTTGGTGTGAGGAACTCAAGAGCTTCACCTTCTACCGGAGGGACATGGGCT 320
 Db 272 CCTGAGGGAGAACAGAAGAGCAGGACAAAGCCTTCATCCGGCTCAGAGTGGCC 331

Qy 321 CACCTCAGCTTGAGTGGCTACCCGGCTGTTCTGTGACGGGCCCTGAGC 380
 Db 332 CACCACTGTTTGAGTGTGGCTGGCCCTGCCCCGGTTGTCCTGTCAGACGGATGGAGC 391

Qy 381 CGATCAGCTGTCAGACTCACCCAGCTCCCGAGAATGGTGC 423
 Db 392 TGACCAAGCCGTCAGCTCACCAATAATGCCAGCGAGGCCCTC 434

ORIGIN

Query Match 23.5%; Score 110.2; DB 7; Length 615;
 Best Local Similarity 58.8%; Pred. No. 2.3e-19;
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

Qy 24 CTTCCGATGAGGAGCTGGCATGAAAGGTCTTATCTGCTATAAACGCTCTAGC 83
 Db 102 CTCAGAACTGGATCTTAACCAAGAGACCTCTATCTGAGGAGAACCTACTAGTGC 161

Qy 84 TGGAGGCTGTGAGGGAGGTCTTAAGGTGAGAGATCAGCTGGTGGCCCATCG 143
 Db 162 TGGTACTATTCGAGGACCAATGTCATTTAGAGAAAGATAGATGTTGATACCATG 221

Qy 144 GTCGCTGATGCCAGCCATCTGGGTCATCTGGGTCAGGGTGAACCCAGCTGCCT 203
 Db 222 GCTCTCATGCTC-----TGTCTTGGTAACTCATGAGGGAAATGTCCT 266

Qy 204 GTCATGTTGGTGTGAGGAGGACTCTAACATAAGCCAGTCTGAACATCATGGA 260
 Db 267 GTCCTGTCAGTCTGGTGTGAGGAGGACTCTAACATAAGCCAGTCTGAACATCATGGA 326

Qy 261 GTCCTATCTTGGTGTGAGGAACTCAAGAGCTTCACCTTCTACCGGAGGACATGGGCT 320
 Db 327 CCTGAGGGAGAACAGAAGAGCAGGACAAAGCCTTCATCCCTCACAGGGCC 386

Qy 321 CACCTCAGCTTGAGTGGCTACCCGGCTGTTCTGTGACGGGCCCTGAGC 380
 Db 387 CACCACTGTTTGAGTGTGGCTGGCCCTCCCGGCTGTTCTGTGACGGGCCCTGAGC 446

Qy 381 CGATCAGCTGTCAGACTCACCCAGCTCCCGAGAATGGTGC 423
 Db 447 TGACCAAGCCGTCAGCTCACCAATAATGCCAGCGAGGCCCTC 489

RESULT 34

CR94825 CR94825 615 bp mRNA linear EST 28-JUN-2005

DEFINITION CR94825 RZPD no.9016 Homo sapiens cDNA clone RZPDp9016N0622 5',
 mRNA sequence.

ACCESSION CR94825

VERSION CR94825.1 GI:68288710

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

AUTHORS Homo sapiens (human)

REFERENCE Homo sapiens (human)

TITLE Human T-Lymphocytes library

JOURNAL Unpublished (2005)

COMMENT Contact: Inge Arlert
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Helmholtzweg 6, D-14059 Berlin, Germany
 Email: www.rzpd.de

RESULT 35

BI489807 BI489807 864 bp mRNA linear EST 28-AUG-2001

DEFINITION 603015661 NIH_MCC_115 Homo sapiens cDNA clone IMAGE:5172896 5',
 mRNA sequence.

ACCESSION BI489807

VERSION BL489807.1 GI:15329035
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Mammalia; Eutheria; Euarchoptoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 864)
 AUTHORS NIH-MGC
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straubberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Invitrogen Genomics, Inc.
 Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
 Plate: LLAMI430, row: 9, column: 09
 High quality sequence step: 862.

FEATURES source
 Location/Qualifiers
 1. 864
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5172896"
 /lab_host="DHIOB"
 /clone_id="NIH_MGC_115"
 /note="organ: pooled brain, lung, testis; vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site 1 is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
 ORIGIN

Query Match 23.5%; Score 110.2; DB 3; Length 864;
 Best Local Similarity 58.8%; Pred. No. 2.5e-19; Gaps 2;
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

QY 24 CTTCCGATGAAAGGACTCGGCAATTGAAAGGTGCTTATCTGCAATAAACCGCTCTAGC 83
 Db 144 CTCAGAACTGGATGTAAACAGAACCTCTATCTGAGAACACCAACTAGTGC 203
 Qy 84 TGGAGGCTGATGAGGAAAGTCATTAAGGTGAGAGTCAGCTGGTCCCATCG 143
 Db 204 TGGATACCTGAGGACCAATATCTCAATTAGAGAAAGATAGATGTGGTACCCATTGA 263
 Qy 144 GTCGCTGGATGCCAGCCATCTGGGTGAAAGCCAGTCCT 203
 Db 264 GCCTCATGCTC-----TGTCTTGGGATCTCATGGAGAGATGTGCT 308
 Qy 204 GTCATGGGGTG---GGGAGGAGCCACTTAACATAAGCCAGTGAGATCATGGA 260
 Db 309 GTCGCTGGATCTGGTGTAGAGACCACTGAGCTAACATCTGAG 368
 Qy 261 GTCATGGGGTG---GGGAGGAGCCACTTAACATAAGCCAGTGAGATCATGGA 260
 Db 369 CCTGAGGAGAACAGAACAGGAGAACAGCCGCTCGCCTCATCGCTAGAGCGGCC 428
 Qy 321 CACCTCCGCTTGAGTGGCTCTACCGGCTGCTGAGCTCCCTGAG 380
 Db 429 CACCAAGCTTGTAGCTCTGCGACCTGCGCCGTTCTGCAACAGCGATGGAGC 488
 Qy 381 CGATCAGCTGTAGACTCACCCAGCTCCGAGATGTGGC 423
 Db 489 TGACCAAGCCGTCAGCCATATGCCAGACGGCTC 531

FEATURES source
 Location/Qualifiers
 1. 1581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SC0D1086YA15"
 /tissue_type="placenta" Cot 25-normalized"
 /plasmid="pcmvsport_6"
 ORIGIN
 Direct Submission
 Submitted (20/04/2004) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqeff@genoscope.cnrs.fr - Web: www.genoscope.cnrs.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSport 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 FEATURES source
 Location/Qualifiers
 1. 1581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SC0D1086YA15"
 /tissue_type="placenta" Cot 25-normalized"
 /plasmid="pcmvsport_6"
 ORIGIN
 Query Match 23.5%; Score 110.2; DB 4; Length 1581;
 Best Local Similarity 58.8%; Pred. No. 2.8e-9; Gaps 2;
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

QY 24 CTTCCGATGAAAGGACTCGGCAATTGAAAGGTGCTTATCTGCAATAAACCGCTCTAGC 83
 Db 48 CTCAGAACTGGATGTAAACAGAACCTCTATCTGAGAACACCAACTAGTGC 203
 Qy 84 TGGAGGCTGATGAGGAAAGTCATTAAGGTGAGAGTCAGCTGGTCCCATCG 143
 Db 108 TGGATACCTGAGGACCAATGTCAATTAGAGAAAGATAGATGTGGTACCCATTGA 167
 Qy 144 GTCGCTGGATGCCAGCCATCTGGGTGAAAGCCAGTCCT 203
 Db 168 GCCTCATGCTC-----TGTCTTGGGATCTCATGGAGAGATGTGCT 212
 Qy 204 GTCATGGGGTG---GGGAGGAGCCACTTAACATAAGCCAGTGAGATCATGGA 260
 Db 223 GTCGCTGGATCTGGTGTAGAGACCACTGAGCTCCAGCTGGAGATCATGGA 272
 Qy 261 GTCATGGGGTG---GGGAGGAGCCACTTAACATAAGCCAGTGAGATCATGGA 320
 Db 273 CCTGAGGAGAACAGAACAGGAGAACAGCCGCTCGCCTCATCGCTAGAGCGGCC 332
 Qy 321 CACCTCCGCTTGAGTGGCTCTACCGGCTGCTGAGCTCCCTGAG 380
 Db 333 CACCAAGCTTGTAGCTCTGCGACCTGCGCCGTTCTGCAACAGCGATGGAGC 392
 Qy 381 CGATCAGCTGTAGACTCACCCAGCTCCGAGATGTGGC 423
 Db 429 TGACCAAGCCGTCAGCCATATGCCAGACGGCTC 531

Db 393 TGACCAGCCGTCAGCTCACCATATGCCGTAGAGAGGGTC 435

RESULT 37

CR616671 CR616671 full-length cDNA clone CSODM013YB17 of Fetal liver of *Homo sapiens* (human).

DEFINITION full-length cDNA clone CSODM013YB17 of Fetal liver of *Homo sapiens* (human).

ACCESSION CR616671

VERSION CR616671.1 GI:5049748

KEYWORDS HTC; CNSLT cDNA.

SOURCE *Homo sapiens* (human).

ORGANISM *Homo sapiens* (human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1644)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polaves,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue

REFERENCE 2 (bases 1 to 1644)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen

FEATURES

source

1. .1644

/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9606"

/clone="CSODM013YB17"

/tissue type="Fetal liver"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 23.5%; Score 110.2; DB 4; Length 1644; Best Local Similarity 58.8%; Pred. No. 2.8e-19; Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

Qy 24 CTTCCGAATGAGGACTCGGATCTGAAGGTCTTATCTGATATAACCGCTCTAGC 83

Db 118 CTTCAGAACTCTGGATGTAAACAGAGACTCTACTCTGAGAACACCACACTAGTGC 177

Qy 84 TGAGGGCTCATGCAGGAGCTATTAAGGTAAGAGATCAGCGTGGTCCCAATCG 143

Db 178 TGCATACTGCAAGGACAAATGCAATTAGAGAAGAATGATGTGGTACCCATGA 237

Qy 144 GGGCTGATGCCAGCTGTCCTCCCGTCAATTGGGTCTCAGGGTGAAGCAGTCCT 203

Db 238 GCCTCATGCTC-----TGTCTTGGGATCAGTGGAGGAGATGTGCT 282

Qy 204 GTCATGGGGTG---GGGAGGAGGACTCTAACATAGGCCAGTGTGAGATCATGGA 260

Db 283 GTCCTGTTCAACTCTGGTGTGACCTGACGACTTCAGCTGAGGAGCTTAACATCTGA 342

Qy 261 GCTCTATCTGGGCCAGGAATCCAGAGCTAACCTCTACGGGGCATGGGCT 320

Db 343 CCTGAGGGAGAACAGAAGAGGAGAACGCCGCTTACGCTACGGGACATGCC 402

Qy 321 CACCTCCAGCTTGAGTGGCTCGCTCTACCCGACTGGTCTCTGACGGTCTCTGAGC 380

Db 403 CACCACTGGTTGAGTGTGCGCCCTGCCCCGGTGGTCTCTGACAGGGATGGAGC 462

Qy 381 CGATCAGCCTGAGACTCACCCAGCTTCCCGAGAATGTTGG 423

Db 453 TGACCAACCCGTCAGCTCACCATATGCCGTAGAGAGGGTC 505

RESULT 38

CR605915 CR605915 full-length cDNA clone CSODEB01YA17 of Placenta of *Homo sapiens* (human).

DEFINITION full-length cDNA clone CSODEB01YA17 of Placenta of *Homo sapiens* (human).

ACCESSION CR605915

VERSION CR605915.1 GI:50486722

KEYWORDS HTC; CNSLT cDNA.

SOURCE *Homo sapiens* (human).

ORGANISM *Homo sapiens* (human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1656)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polaves,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue

REFERENCE 2 (bases 1 to 1666)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen

FEATURES

source

1. .1666

/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9606"

/clone="CSODEB01YA17"

/tissue type="Placenta"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 23.5%; Score 110.2; DB 4; Length 1666; Best Local Similarity 58.8%; Pred. No. 2.8e-19; Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

Qy 24 CTTCCGAATGAGGACTCGGATCTGAAGGTCTTATCTGATATAACCGCTCTAGC 83

Db 123 CTTCAGAACTCTGGATGTAAACAGAGACTCTACTCTGAGAACACCACACTAGTGC 182

Qy 84 TGAGGGCTCATGCAGGAGCTATTAAGGTAAGAGATCAGCGTGGTCCCAATCG 143

Db 183 TGCATACTGCAAGGACAAATGCAATTAGAGAAGAATGATGTGGTACCCATGA 242

Qy 144 GGGCTGATGCCAGCTGTCCTCCCGTCAATTGGGTCTCAGGGTGAAGCAGTCCT 203

Db 243 GCCTCATGCTC-----TGTCTTGGGATCAGTGGAGGAGATGTGCT 287

Qy 204 GTCATGGGGTG---GGGAGGAGGACTCTAACATAGGCCAGTGTGAGATCATGGA 260

Db 288 GTCCTGTTCAACTCTGGTGTGACCTGACGACTTCAGCTGAGGAGCTTAACATCTGA 347

Qy 261 GCTCTATCTGGGCCAGGAATCCAGAGCTAACCTCTACGGGGCATGGGCT 320

Db 348 CCTGAGGGAGAACAGAAGAGGAGAACGCCGCTTACGCTACGGGACATGCC 407

Qy 321 CACCTCCAGCTTGAGTGGCTCGCTCTACCCGACTGGTCTCTGACGGTCTCTGAGC 380

Db 408 CACCACTGGTTGAGTGTGCGCCCTGCCCCGGTGGTCTCTGACAGGGATGGAGC 467

Qy	381 CGATCGCCCTCGAGCTCACCCAGCTTCCCGAGAAATGGTGGC 423	Qy	144 GTGGCTGAGTGCACGCCCTGTCAGGCTGAGCCAGTGCC 203
Db	468 TGACCAGCCCCCTAGCTCACCAATGCTGACGAGGCC 510	Db	261 G-----CTGATGCTCTATTCTGGGACATGGCATGGAGGCTG 305
RESULT 39		Qy	204 GTCATGTCGAGCTGAGGAGCCGACTCTAACATAGAGCCAGTGACATGG 260
LOCUS	CD468528 735 bp mRNA linear EST 04-JUN-2003	Db	306 GGCTCTGTCAAGTCAGTCGATGATGATTGGATGAGCTGCTG 365
DEFINITION	Leukos3_3_D10_91_A025 Stimulated peripheral blood leukocytes S3	Qy	261 GCTCTACTTGTGCGCAAGGATCCAGACTTCACTTACAGCTTACGGCT 320
ACCESSION	Equus caballus cDNA clone Leukos3_3_D10_A025 5, mRNA sequence.	Db	366 CCTGAGCAAGACAGGGAGGAGAACAGACCTTCAACAGCTGCC 425
VERSION	CD468528	Qy	321 CACCTCCAGCTCGAGTCGAGCTGCCTACCGGGCTGGTCTGTGAGCG 380
KEYWORDS	EST	Db	426 CACCAACAGCTCGAGCTGCCTGGCTGGTCTCTCTGCAAGCGGCC 485
SOURCE	Equus caballus (horse)	Qy	381 CGATCGCCCTCGAGCTCACCCAGCTTCCGGAGATGTTGGTGTGAGC 440
ORGANISM	Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Laurasitheria; Perissodactyla; Equidae; Equus.	Db	486 AGACCGCTTCAGCCACACAGAGCCCTCAGAGGGAGTACAGGAGCCTG 545
REFERENCE	1 (bases 1 to 735); Vandemerg, M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., More,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.	Qy	441 AGACTCTACTTCCAGC 457
AUTHORS	An EST database from equine (Equus caballus) stimulated peripheral blood leukocytes	Db	546 AGGACTCTGTCAGC 562
TITLE	Unpublished (2003)	COMMENT	
JOURNAL	Contract: Cordonnier-Pratt MM	FEATURES	
COMMENT	Laboratory for Genomics and Bioinformatics	source	
	The University of Georgia, Department of Plant Biology		
	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA		
	Fax: 706 542 1860		
	Email: impratt@uga.edu		
FEATURES			
source			
RESULT 40		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	Qy	
	1 (bases 1 to 572)	Qy	
FEATURES		Qy	
source		Qy	
RESULT 41		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 42		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 43		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 44		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 45		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 46		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 47		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 48		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 49		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 50		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 51		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 52		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 53		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 54		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 55		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 56		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (human)	Qy	
REFERENCE		Qy	
AUTHORS		Qy	
	Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Drlic,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequeira,R., Book,S., Doucette-Stamm,L., Le Peuch,C., Vandenhoute,J., Cusick,M.E., Albla,J., Hill,D.E. and Vidal,M.	Qy	
FEATURES		Qy	
source		Qy	
RESULT 57		Qy	
LOCUS	CV027812 572 bp mRNA linear EST 20-AUG-2004	Qy	
DEFINITION	CV027812 614 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5', similar to BC009745, mRNA sequence.	Qy	
ACCESSION	CV027812	Qy	
VERSION	CV027812.1 GI:51485880	Qy	
KEYWORDS	EST	Qy	
SOURCE		Qy	
ORGANISM	Homo sapiens (

was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1388.f. For more information about this cluster, see <http://www.genoscope.cnrs.fr/cdns?cs=CC0AM013AC05QP1&c=1388.f>.

FEATURES

source

1. .932
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SD0M013YE17"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: PCMVSPORT_6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRI sites of the PCMVSPORT_6 vector. Library was not normalized."

ORIGIN

Query Match 23.2%; Score 108.6; DB 5; Length 932;
 Best Local Similarity 58.6%; Pred. No. 7e-19; Mismatches 149; Indels 18; Gaps 2;
 Matches 236; Conservative 0; MisMatches 149; Index 18; Gaps 2;
 Qy 24 CTTCCGATGAGGACTCGGATGAGGTCTTATCGATAATAACCGCTCTAGC 83
 Db 118 CTCAGATCTGGATTTAACAGAGACCTCTCTGGAGAACATCAGTTGC 177
 Qy 84 TGGAGGCTGGATGCGGGAGGCTTAAGGTGAGAGTCASCGTGTGGCCATAGC 143
 Db 178 CGGATACTGGAGGCTTAAGGTGAGAGTCASCGTGTGGCCATAGC 237
 Qy 144 GTGGCTGGATGCCAGCTGTCCCCGTCATCTGGGTGTCAGGTCAGCAGTGCCT 203
 Db 238 GCTCTATGTC-----TGTCTTGTGAAATCCATGAGGGAGATGTCCT 282
 Qy 204 GTCATGTTGGCTG---GGGCAGGAGCCACTTAACACTAGAAGCCAGTGAACATCGGA 260
 Db 283 GTCCTGTTCAAGTCTGTGATGAGACAGCTCCACCTGGAGGCACTTAACATCGA 342
 Qy 261 GCTCTATCTTGTCGCAAGGAGATCCAGAGCTCACCTCACCGGGCATGGCT 320
 Db 343 CCTGAGCGAGACAGAACAGACAGACAGACAGTCAGTGAGGCC 402
 Qy 321 GACCTCGAGCTTGAGTGGCTAACCGGCTGGTCTCTGGACGGCTCTGAAGC 380
 Db 403 CACGACGATTGTGAGCTGGCTCCCGCTGGTCTCTGTCAGCAGGATGAGC 462
 Qy 381 CGATCAGCTGAGACTCACCCAGCTCCCGAGAATGGTGC 423
 Db 463 TGACCAAGCCGTCAGCCTACCAATACTCTGAGAAGGCC 505

RESULT 43

BE563703
 LOCUS BE563703 938 bp mRNA linear EST 15-AUG-2000
 DEFINITION 6013532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689284 5',
 mRNA, Beutner.

ACCESSION BE563703

VERSION BE563703.1

EST. BE563703

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: <http://image.lnl.gov>

FEATURES

source

1. .938
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:369284"
 /tissue_type="denocarcinoma"
 /lab_host="DH10B (phage-resistant)"

FEATURES

source

/note="Organ: pancreas; vector: pOTB7; site: 1: XbaI;
 Site: 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XbaI sites using the following adaptor: GGCACGAG (G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

source

Query Match 23.2%; Score 108.6; DB 2; Length 938;
 Best Local Similarity 58.6%; Pred. No. 7e-19; Mismatches 149; Indels 18; Gaps 2;
 Matches 236; Conservative 0; MisMatches 149; Index 18; Gaps 2;

Qy 24 CTTCCGATGAGGACTCGGATGAGGTCTTATCGATAATAACCGCTCTAGC 83
 Db 127 CGGATACTGGATGAAAGACAAATGTCAATTAGAAGAAGATAGTGTGATACCATTGA 186
 Qy 67 CTTCAGATCTGGATGTTAACAGAGAACCTCTCTGAGGAAACACCAACTAGTGC 126

Qy 84 TGGAGGCTCATGAGGGAGGTCATAAAGGTGAGAGTCACGCTGTGGCTCAGGTTGAGCCAGTGCCT 143
 Db 144 GTGGCTGGATGCCAGCGTGTCCCCCTCATCTGGGTGTCAGGTTGAGCCAGTGCCT 203
 Qy 187 GCCTCATGTC-----TGTCTTGTGAGATCATGGAGGAGATGTCCT 231

Db 204 GTCATGTTGGCTG---GGGCAGGAGCCACTTAACACTAGAAGCCAGTGAACATCGGA 260

Qy 232 GTCCTGTTCAAGTCTGTGATGAGACAGCTCACGCTGGAGGAGCTAACATCGA 291

Db 261 GCTCTATCTTGTCGCAAGGATTCAGAGCTCACCTTCACCCGGGACATGGCT 320

Qy 292 CCTGAGCGAGACAGAACAGACAGACAGACAGACAGCTGGCTCAGACAGTGAGGCC 351

Db 321 CACCTCGAGCTTGAGTGGCTAACCGGCTGGTCTCTGTCAGCAGGTCCTGAAGC 380

Qy 352 CACCAACAGTTTGACTCTGCCGCTCCCGGTTGGTCTCTGCAAGCGATGGAGC 411

Db 381 CGATCAGCTGAGACTCACCCAGCTCCCGAGAATGGTGC 423

Db 412 TGACCAAGCCGTCAGCCTACCAATGTCGAGAAGGCC 454

RESULT 44

BM009048
 LOCUS BM009048 955 bp mRNA linear EST 30-OCT-2001
 DEFINITION 60318892F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:5422918 5',
 mRNA sequence.

ACCESSION BM009048

VERSION BM009048.1

EST. GR:16523402

Homo sapiens (human)

Homo sapiens (human)

COMMENT

Email: cgabs-r@mail.nih.gov

REFERENCE

1 (bases 1 to 938)

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Robert Strauberg, Ph.D.

COMMENT

AL554778	RESULT 46	Db	393	TGACCGAGCCCCCTCAGCTCAATGCTGACGAGGCTC 435	
LOCUS	AL554778	DEFINITION	1069 bp mRNA linear EST 30-MAR-2004		
ACCESSION	AL554778.8	VERSION	Homo sapiens PLACENTA COT 25-NORMALIZED	Homo sapiens cDNA	
SOURCE	clone CSOD10867A15	KEYWORDS	5'-mRNA sequence.		
ORGANISM	Homo sapiens	COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butchera; Euarachontoglires; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.	REFERENCE	1 (bases 1 to 1069)		
TITLE	Full-length cDNA libraries and normalization	AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.		
JOURNAL	Unpublished (2001)	COMMENT	On Feb 15, 2001 this sequence version replaced gi:31276588.		
FEATURES	source	ORGANISM	Homo sapiens (human)		
ORIGIN	Genoscope	REFERENCE	1 (bases 1 to 1069)		
Query Match	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE	AUTHORS	Genoscope		
Best Local Similarity	Email: seqref@genoscope.cns.fr	COMMENT	1 (bases 1 to 1069)		
Matches	58.3%; Pred. No. 9.3e-19;保守性 1; Mismatches 149; Indels 18; Gaps 2;	TITLE	Genoscope National de Sequencing		
Qy	235	JOURNAL	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
24	CTTCGGAATGAGGGCTCGGGATTGAGGCTCTTATCTGATAATAAACAGCTCTAGC 83	COMMENT	1 (bases 1 to 1069)		
48	CTTCGAGAACATCTGGAGCTTAACCAAGAACCTCTATCTGAGGACAACTAGTGC 107	ORGANISM	Homo sapiens (human)		
84	TGGAGGGCTGTAGCAGGGAGGTCTTAAGGTTGAGAGATCAGCTGGTCCCATTG 143	REFERENCE	1 (bases 1 to 1069)		
108	CGGATACATTCGAGGACCAATTCTCAATTAGAAGAAAGTAGATGGTACCCATG 167	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butchera; Euarachontoglires; Primates; Catarrhini; Homiidae; Homo.		
Qy	144	FEATURES	1 (bases 1 to 1069)		
Db	GTGGCTGGATGCCAGACTGTCCCCGTCATCCTGGGTCAGGAGATGTCCT 203	source	1 (bases 1 to 1069)		
Db	168 GCCTCATGCTC-----TGTCTTGGAATCATGGAGGATGTCCT 212	ORGANISM	Homo sapiens (human)		
Qy	204 GTCATGTGGGTG-----GGCAGGAGCCACTAACCTAGGGCCTGACATCTGGA 260	REFERENCE	1 (bases 1 to 1069)		
Db	213 GTCAGCTGGTCAAGTCTGGTGTAGGAAGCAGACTCCACTGAGGAGGT 272	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butchera; Euarachontoglires; Primates; Catarrhini; Homiidae; Homo.		
Qy	261 GCTCTATCTTGGGCCAGGANTCAGAGCTTACCTTCTACCGGGAGATG 320	COMMENT	1 (bases 1 to 1069)		
Db	273 CCTGAGGGAGAACGAAGAGCAGCAAGGCTCTGCTCATCCGTCAGAGTGGCC 332	TITLE	Genoscope National de Sequencing		
Qy	321 CACCTCCAGCTGAGTGGCTCTACCCGGCTGGTCAGGGCTCTGAGGCT 380	JOURNAL	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
Db	333 CACCAACGAGTTGTGAGTGGCTCTGCGCTCTGCCGGTGTGGCTCTGCAACGATGGAGC 392	COMMENT	1 (bases 1 to 1069)		
381 CGATCAGCTGTCAGACTAACCGAGCTCCGGAGAATGGTGGC 423	FEATURES	source	1 (bases 1 to 1069)		
ORIGIN	Query Match	Query Match	Query Match	Query Match	
Best Local Similarity	23.1%; Score 108.2; DB 1; Length 1069;	Best Local Similarity	22.9%; Score 107; DB 3; Length 403;	Best Local Similarity	22.9%; Score 107; DB 3; Length 403;
Matches	235; Conservative 1; Mismatches 149; Indels 18; Gaps 2;	Matches	226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;	Matches	226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;
Qy	1.1069 organism="Homo sapiens"	Qy	1.1069 organism="Homo sapiens"	Qy	1.1069 organism="Homo sapiens"
/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"	/mol_type="mRNA"
/db_xref="taxon:9606"	/clone=CSOD10867A15"	/db_xref="taxon:9606"	/clone=CSOD10867A15"	/db_xref="taxon:9606"	/clone=CSOD10867A15"
/tissue_type="PLACENTA COT 25-NORMALIZED"					
notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1388.f. For more information about this cluster, see http://www.genoscope.cns.fr/cdns/s=CSOD10867A00QP1&c=1388.f.	notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN	Query Match				
Best Local Similarity	58.3%; Pred. No. 9.3e-19;保守性 1; Mismatches 149; Indels 18; Gaps 2;	Best Local Similarity	59.6%; Pred. No. 1.6e-18;保守性 0; Mismatches 135; Indels 18; Gaps 2;	Best Local Similarity	59.6%; Pred. No. 1.6e-18;保守性 0; Mismatches 135; Indels 18; Gaps 2;
Qy	1.1069 organism="Homo sapiens"	Qy	1.1069 organism="Homo sapiens"	Qy	1.1069 organism="Homo sapiens"
/mol_type="mRNA"	/clone=CSOD10867A15"	/mol_type="mRNA"	/clone=CSOD10867A15"	/mol_type="mRNA"	/clone=CSOD10867A15"
/db_xref="taxon:9606"	/db_xref="taxon:9606"	/db_xref="taxon:9606"	/db_xref="taxon:9606"	/db_xref="taxon:9606"	/db_xref="taxon:9606"
/clone="S07T665307-5-D12"	/clone="S07T665307-5-D12"	/clone="S07T665307-5-D12"	/clone="S07T665307-5-D12"	/clone="S07T665307-5-D12"	/clone="S07T665307-5-D12"
/sex="M"	/sex="M"	/sex="M"	/sex="M"	/sex="M"	/sex="M"
/lab_host="Top10F"	/lab_host="Top10F"	/lab_host="Top10F"	/lab_host="Top10F"	/lab_host="Top10F"	/lab_host="Top10F"
/clone_id="S07T665307"	/clone_id="S07T665307"	/clone_id="S07T665307"	/clone_id="S07T665307"	/clone_id="S07T665307"	/clone_id="S07T665307"
note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Db	128	-TGTCTCTGGGATCCATGAGGGAGATGTCCTGTCAGTCTGTTGTA	185	Db	62	CATTTAGAGAAAGATAGATGTGAAACCATGAGCCTCATGCTC-----	108
Qy	225	GCGGACTCTAACCTAGAGCAGCTGAACATCAGGAGCTCTACCTTGCTGCGGAGGATC	284	Qy	168	CGTCATCTGGGTCAGGGGAAACCAAGCTCTCATGG--GGTGGGGAGGA	224
Db	186	GACGAGACTCCAGCTGGAGGAGCTACATCTACTGACCTGAGACAGAAAGCAGGA	245	Db	109	--TGTCTCTGGGATCCATGAGGGAGATGTCCTGCGCTCTGTCAGTCAGTGTA	166
Qy	285	CGAGACTCACCCTCACCGGGAGCATGGGCTCACCTCCAGCTCGAGTCGGCTGC	344	Qy	225	GCGGACTCTAACCTAGAGCAGCTGAACATCAGGAGCTCTCATGG--GGTGGGGAGGA	284
Db	246	CGAGCCTCTGCTTCATCCGCTCACAGCGCCACCCACCAAGCTTGAGCTGCGC	305	Db	167	GACGAGACTCAGCTGGAGGAGCTACATCTACTGACCTGAGACAGAAAGCAGGA	226
Qy	345	CTAACCGGGCTGGTCCCTGCAAGGGTCCCTGAGCCATCAGCTGTCAGACTCACCA	404	Qy	285	CGAGACTCACCCTCACCGGGAGCATGGGCTCACCTCCAGCTCGAGTCGGCTGC	344
Db	306	CCTCCCGGGTTGTTCCCTGCAAGGGTCCCTGAGCCATCAGCTGTCAGACTCACCA	365	Db	227	CGAGCCTCTGCTCACCTGGCTCACAGCGCCACCCACCAAGCTTGAGCTGCGC	286
Qy	405	GCTTCCCGAGAATGGTGC	423	Qy	345	CTAACCGGGCTGGTCCCTGCAAGGGTCCCTGAGCCATCAGCTGTCAGACTCACCA	404
Db	366	TATGCCCTGACGAAGGGC	384	Db	287	CTGCCCGGGTGGTCTCTGCAAGGGTCCCTGAGCCCTCAGCCTCACCA	346
RESULT 48							
LOCUS	BG288795	640 bp mRNA linear EST 21-FEB-2001		LOCUS	BG288795	6028812671 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4516927 5,	
DEFINITION				DEFINITION			
ACCESSION	BG288795			ACCESSION	BG288795		
VERSION	BG288796.1	GI:13043994		VERSION	BG288796.1	GI:13043994	
KEYWORDS				KEYWORDS			
SOURCE				SOURCE			
REFERENCE				REFERENCE			
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
FEATURES				FEATURES			
source				source			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			
COMMENT				COMMENT			
ORGANISM				ORGANISM			
REFERENCE							
AUTHORS				AUTHORS			
TITLE				TITLE			
JOURNAL				JOURNAL			
PUBLISHED				PUBLISHED			

tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 22.2%; Score 103.8; DB 2; Length 120;
Best Local Similarity 96.7%; Pred. No. 1.3e-17; P-Match 116; Conserv. 0; Mismatches 3; Indels 1; Gaps 1;
Matches 116; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 105 GGGTCAATTAAGGTGAGAGATCAGCTGGTCCAGGCGGCTATCGGTGGCTGATG-CCAGCTGT 163
Db 1 GGGTCAATTAAGGTGAGAGATCAGCTGGTCCAGGCGGCTATCGGTGGCTGATG-CCAGCTGT 60
Qy 164 CCCCCGGTCATCTGTGGTCCAGGGGGGAGGCCAGTGCCCTGCTCAATGTGGGGTGGGGCAGG 223
Db 61 CCCCCGGTCATCTGTGGTCCAGGGTGGAGGCCAGTGCCCTGCTCAATCGGGCTGGGGCAGG 120

Search completed: January 27, 2006, 21:51:48
Job time : 3090 sec

RESULT 50

LOCUS DQ043278 435 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL1F10 gene, VIRTUAL TRANSCRIPT, Partial sequence,
genomic survey sequence.

ACCESSION DQ043278

VERSION DQ043278.1 GI:66994493

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 435)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glianowski, S., Sackton, T. B., Hubisz, M.J., Pledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpazees
JOURNAL PLoS Biol. 3 (6), e170 (2005)

REFERENCE 2 (bases 1 to 435)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glianowski, S., Sackton, T. B., Hubisz, M.J., Pledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES location/Qualifiers 1. 435
source /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
<1..>435
<1..>IL1F10"
/gene="IL1F10"
/locus_tag="HC10058"

ORIGIN

Query Match 22.2%; Score 103.8; DB 11; Length 435;
Best Local Similarity 62.2%; P-Match. No. 1.3e-17; P-Match 181; Conserv. 0; Mismatches 107; Indels 3; Gaps 1;
Matches 118 GAGAGATCAGCTGGTCCCAATCGGGGGTGGATGCCAGCTGGTCCCTCATCTG 177
Db 94 GAGAGATCAGCTGGTCCCAATCGGGGGTGGATGCCAGCTGGTCCCTCATCTG 153
Qy 178 GGGTCAATTAAGGTGAGAGATCAGCTGGTCCAGGCGGCTGCTGAGGCTCAATCGGTGGCTGATG-CCAGCTGT 234
Db 154 GGGTCAATTAAGGTGAGAGATCAGCTGGTCCAGGCGGCTGCTGAGGCTCAATCGGTGGCTGATG-CCAGCTGT 213
Qy 235 ACTAGAGCCAGTGAACATCATGGAGTCATCTGTGGTCCAGGAATCTTCAAGAGCTTC 294

Db 214 CAGCTGGAGGATGTGAACTGAGGAACTGTACAAGTGGTGAAGGGCACACGCTTC 273
Qy 295 ACCTCTACGGCGGAGATGGGCTCCTCCAGCTGAGTGGCTCTAACCAGGC 354
Db 274 ACCTCTACGGCGGAGATGGGCTCCTCCAGCTGAGTGGCTCTAACCAGGC 333
Qy 355 TGGTCCCTGGCACGGTGCCTGAAGCCGATCAGCTGTGAGACTCACCCAG 405
Db 334 TGGTCCCTGGCACGGCAGACCCAGCAGCACAGCTCACACANG 384